

STE20_h	MAH	LRGF	ANQHS	RV	---	DPEEL	FTKL	DR	IGKGS	FGEV	YK	GIDN	HTK	43
MST3_h	MAH	SPVQ	SGLP	GMQNL	KA	DPEEL	FTKL	EK	IGKGS	FGEV	FK	GIDN	RTQ	47
STLK2_h	MAH	SPVAV	QVP	GMQNN	IA	DPEEL	FTKL	ER	IGKGS	FGEV	FK	GIDN	RTQ	47
STLK3_h	TA	APAA	PAPAA	PAQA	AVGW	PICR	DAYEL	Q	EV	IGS	ATAV	VQAAL	CKPRQ	57
STE20_h	EV	VAIK	II	DL	EEA	EDE	IED	IQ	EEIT	VL	SQ	CD	SPY	100
MST3_h	KV	VAIK	II	DL	EEA	EDE	IED	IQ	EEIT	VL	SQ	CD	SPY	104
STLK2_h	QV	VAIK	II	DL	EEA	EDE	IED	IQ	EEIT	VL	SQ	CD	SPY	104
STLK3_h	ER	VAIK	RI	NLE	KCQ	TSM	DEL	LKE	IQ	AM	SQ	CS	HPN	114
STE20_h	GS	AL	DL	L	K	P	G	P	---	---	---	---	---	148
MST3_h	GS	AL	DL	L	E	P	G	P	---	---	---	---	---	152
STLK2_h	GS	AL	DL	L	R	A	G	P	---	---	---	---	---	152
STLK3_h	GS	ML	D	II	K	Y	I	V	N	R	G	E	H	171
STLK4_h	---	---	---	---	---	---	---	---	---	---	---	---	---	41
STE20_h	SE	Q	G	D	V	K	L	A	D	F	G	V	---	198
MST3_h	SE	H	G	E	V	K	L	A	D	F	G	V	---	202
STLK2_h	SE	Q	G	D	V	K	L	A	D	F	G	V	---	202
STLK3_h	G	E	D	G	S	V	Q	I	A	D	F	G	V	227
STLK4_h	G	E	D	G	S	V	Q	I	A	D	F	G	V	97

Fig. 1A



STE20_h	RQ--PRSQCLSTLVRPVPVFGELKEKHKQSGGSGVGALEEL ENAFSLAEE SCPGISDKLM	405
MST3_h	IPKRPFSCCLSTIISPLFAELKEKSKQACGGNLSIEELRGAIYLAEEACPGISDTMV	411
STLK2_h	-----CLSMIITPAFAELKQQDENNASRNQAI EEL EKSI AVAEEACPGITDKMV	400
STLK3_h	DY--REASSCAVNLVLRNLSRKEINLDIRFEFTPGRDTADGVSSQELF SAGLVDGHDV	468
STLK4_h	-----ISLVLRNLSKKEINLDIRFEFTPGRDTAEGVSSQELI SAGLVDGRDL	366
STE20_h	VHLVERVQRFSHNRRNHLTSTR	426
MST3_h	AQLVQRLQRYSLSGGGTSSH	431
STLK2_h	KKLIEKFQKCSADESP	416
STLK3_h	VIVAAANLQKIVDDPKALKTLTFKLASGCDGSEIPDEVKLI GF AQLSVS	516
STLK4_h	VIVAAANLQKIVEEPQSNR[SVTFKLASGVEGSDIPDDGKLI GF AQLSIS	414

Fig. 1C

Ste20_h	MAHLRG.FANQHSRV	- - - - - DPEELFTKLRIGKGSFG	EYVKGI	DNH	TIK	43
T19A5.2_ce	MTTSSDELPRQADD	SMMKWDRYYIQKLDPEVIFTKQERIGRGSFG	EYVKGI	DNR	TIG	57
Pak_sp	- - - - -	- - - - - LLYRNFFVKIGGASGDVYSARQVG	TIN			26
STLK5_h	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	0
Ste20_h	EVVAIKIIDLEEADEIEDIQQEITVTLSQCDSPIYTRYFGSYLKSTKLWIIIMEYLGG					100
T19A5.2_ce	RVVAIKIIDLEQAEDIEDIQQEIQTVLVSQCDSQYVTKYFGSFLKSGSKLWIIIMEYLGG					114
Pak_sp	LSVAIKKMNIHQPKKEF-IIVNEILVMKSHHKNIVNFIDTFYKSELWMVMEYMRG					82
STLK5_h	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	0

Protein	Sequence	Position
Ste20_h	GSA L D L L K P G P L E E T Y I A T I L R E I L K G L D Y L H S E R K I H R D I K A A N V L L S E Q G D V K L I A	157
T19A5.2_ce	GSA L D L T K S G K L D E S H I A V I L R E I L K G L E Y L H S E R K I H R D I K A A N V L V S E H G D V K V A	171
Pak_sp	GSL T E V V T N N T L S E G Q I A A I C K E T L E G L Q H L H E N G I V H R D I K S D N I L L S L Q G D I K L I T	139
STLK5_h	-- L I C T H F M D G M N E L A I A Y I L Q G V L K A L D Y I I H M G Y V H R S V K A S H I L I S V D G K V Y L S	55

Ste20_h	D F G V A G Q L T D T Q I K R N T F V G T P F - - - - - W M A P E V I K Q S A - - Y D F K A D I W S L G I T A	205
T19A5.2_ce	D F G V A G Q L T E T V K K R I T F V G S P F - - - - - W M A P E L I K Q S S - - Y D Y K A D I W S L G I T A	219
Pak_sp	D F G F C A Q I D S N M T K R T I M V G T P Y - - - - - W M A P E V V T R K E - - Y G F K V D V W S L G I M A	187
STLK5_h	G L R S N L S M I S A G Q R Q R V V H D F P K Y S V K V L P W L S P E V L Q Q N L Q G G Y D A K S D I I Y S V G I T A	112

Protein	Sequence	Position
Ste20_h	I E L A K G E P P N S D L H P M R V L F L I P K - N S P P T L E G - Q - - - - -	238
T19A5.2_ce	I E L A N G E P P H S D L H P M R V L F L I P K - N P P P V L Q G S Q - - - - -	253
pak_sp	I E M V E G E P P Y L N E N P L R A L Y L I A T I G T P K I S R P E L - - - - -	222
STLK5_h	C E L A N G H V P F K D M P A T Q M L L E K L N - G T V P C L D - T S T I P A E E L T M S P S R S V A N S G L S	167



ZC504.4\_ce

NIK\_m

ZC1\_h

ZC2\_h

ZC3\_h

MISSGGEDE--IDLNSLRDPAGIFELIEVVGNNGTYGQVYKGRHVKTALQLAAIKIMININE58  
MANDSPAKSLVDIDLSSLRDPAGIFELVEVVGNNGTYGQVYKGRHVKTVT-AAIKVMDVTE69  
MANDSPAKSLVDIDLSSLRDPAGIFELVEVVGNNGTYGQVHGRHVKTGQLAAIKVMDVTE60  
-----AFGEVYEGRHKVTGQLAAIKVMDVTG28  
-----AFGEVYEGRHKVTGQLAAIKVMDVTE28

ZC504.4\_ce

NIK\_m

ZC1\_h

ZC2\_h

ZC3\_h

DEEDEIKLEINMLKKHSHHRNVATYYGAFIKKLPSSTGKHQDLWLVMFCGSGSITDLVK116  
DEEEITLEINMLKKYSHHRNIATYYGAFIKKSPPGHD--DQLWLVMFCGAGSITDLVK117  
DEEEIKLEINMLKKYSHHRNIATYYGAFIKKSPPGHD--DQLWLVMFCGAGSITDLVK118  
DEEEIKQLEINMLKKYSHHRNIATYYGAFIKKNPPGMD--DQLWLVMFCGAGSVTDLIK84  
DEEEIKQLEINMLKKYSHHRNIATYYGAFIKKSPPGND--DQLWLVMFCGAGSVTDLVK84

ZC504.4\_ce

NIK\_m

ZC1\_h

ZC2\_h

ZC3\_h

NTKGGSLKEEWIAYICREILRGLYHLHQSKVIHRDIKQNVLLTDSAEVKLVDFGVSAQL176  
NTKGNTLKEDWIAIYSREILRGLAHLHIHHV IHRDIKQNVLLTENA EVKLVDFGVSAQL177  
NTKGNTLKEDWIAIYSREILRGLAHLHIHHV IHRDIKQNVLLTENA EVKLVDFGVSAQL178  
NTKGNTLKEDWIAIYSREILRGLAHLHIHHV IHRDIKQNVLLTENA EVKLVDFGVSAQL144  
NTKGNTLKEDWIAIYSREILRGLAHLHIHHV IHRDIKQNVLLTENA EVKLVDFGVSAQL144

ZC504.4\_ce

NIK\_m

ZC1\_h

ZC2\_h

ZC3\_h

DKTVGRRNTFIGTPYWMapevIACDESPPEATYDSRSDLWSLGITALEMAEGHPPLCDMHP236  
DRTVGRRNTFIGTPYWMapevIACDENPDATYDRSDLSWCCGITAIEMAEGGPPPLCDMHP237  
DRTVGRRNTFIGTPYWMapevIACDENPDATYDRSDLSWCCGITAIEMAEGAPPLCDMHP238  
DRTVGRRNTFIGTPYWMapevIACDENPDATYDFKSDLSWLGITAIEMAEGAPPLCDMHP204  
DRTVGRRNTFIGTPYWMapevIACDENPDATYDRSDTWLSLGITAIEMAEGAPPLCDMHP204

Fig. 3A

ZC504.4\_ce

NIK m

417Z

4-27

ZC3\_h

ZC504.4\_ce

NIK m

ZC1\_h

7C2 h

ZC3 h

ZC504.4\_ce

NIK\_m

ZC1\_h

7C2\_h

ZC3\_h

ZC504.4\_ce

NIK\_m

41Z

ZC2\_h

ZC3\_h

**Fig. 3B**





ZC504.4_ce	-----NSGHGAYKGKKIPEIRPGIISL-DDDDSD	623
NIK_m	-----AWSRSDSDEVPRVPVVRTTSRSPVLSRRD	639
ZC1_h	-----PQVPVRTTSRSPVLSRRD	648
ZC2_h	NSDPTSENPPPLPTRIEKFDRSSWLQEEIIPKVPQRTTISISPAIARKN	635
ZC3_h	NSDPTSEGGPSPNPP-----AWVRPD-NEAPPKVPQRTSSIAATALNTSGAGGSRPAQAVR	689
ZC504.4_ce	SDNE-----EGNEPLMFKPIVRCPSIFFWFLS---	651
NIK_m	QAGQ-----RNSTSIEPRLLWERVEKLVPRPG--	667
ZC1_h	SQAG-----QRNSTSIEPRLLWERVEKLVPRPG--	676
ZC2_h	LGSQ-----PIRASNPDLRRTTEPILESPLRQRTSSSG	665
ZC3_h	ARPRSNSAWQIYLQRRRAERGTPKPPGPAQPPPPNASNPDLRRSDPG-----WERS---	742
ZC504.4_ce	--ANVIHSVDGSIPLVKHLIWFQNASRRGALPDLLPKSPCLRRQINDQTRQMSDDRADE	709
NIK_m	--SGSSSGSSNSGSPGSGNPGSQSGSGERFVRSSSKSEGGSPSPRQESAAKKPDDKKEVF	725
ZC1_h	--SGSSSGSSNSGSPGSGHPGSGSQSGGERFVRSSSKSEGGSPSPRQENAVKKPEDKKEVF	734
ZC2_h	SSSSSTPSQPSQSGSQSGSQAGSERTVRANNSKSEGGSPVLPHEPAKVKPEESRDIT	725
ZC3_h	--DSVLPASHGHLP-----QAGSLERNRVGVSSKPDSSPVLSPGNKAKPDDHRSRPG	792
ZC504.4_ce	QPNGFQ-----NSDSR-----SSIQHSFSNRDREKSFVGYFGGGAGAGGTVNRPG---	755
NIK_m	RSCLKPAgev-----DLTAL-----AKELRAVEDVRPPHKVTDYSSSSEESGTTDEEEEDVED	777
ZC1_h	RPLKPA-----DLTAL-----AKELRAVEDVRPPHKVTDYSSSSEESGTTDEEEEDVED	783
ZC2_h	RPSRPA SYKKAIDE DLTAL AKELRELRIEETNRPMKKVTDYSSSSEESSESSEEEEDGES	785
ZC3_h	RPADFV-----L-----LKERTLDEAPRPPKKAMDYSSSSEESSESSEDDEEEEGEG	837

Fig. 3D

ZC504.4_ce	EGADDS	TS	GP	ED	TR	AA	SS	PN	LS	NG	ET	ES	VK	TM	IV	HD	DV	VE	SE	PAM	TP	--	SK	EG	TL	IV	--	755
NIK_m	EGADES	TS	GP	ED	TR	AA	SS	LN	LS	NG	ET	ES	VK	TM	IV	HD	DV	VE	SE	PAM	TP	--	SK	EG	TL	IV	--	831
ZC1_h	ETHD	GT	VA	VS	DI	PR	LI	PT	GA	PS	NE	QY	NV	GM	VG	TH	GL	ET	SH	AD	SF	SG	SI	SR	EG	TL	MIRE	837
ZC2_h	GPA	EGS	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	845	
ZC3_h	GPA	EGS	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	885	
ZC504.4_ce	EGADDS	TS	GP	ED	TR	AA	SS	PN	LS	NG	ET	ES	VK	TM	IV	HD	DV	VE	SE	PAM	TP	--	SK	EG	TL	IV	--	755
NIK_m	EGADES	TS	GP	ED	TR	AA	SS	LN	LS	NG	ET	ES	VK	TM	IV	HD	DV	VE	SE	PAM	TP	--	SK	EG	TL	IV	--	845
ZC1_h	ETHD	GT	VA	VS	DI	PR	LI	PT	GA	PS	NE	QY	NV	GM	VG	TH	GL	ET	SH	AD	SF	SG	SI	SR	EG	TL	MIRE	851
ZC2_h	GPA	EGS	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	905	
ZC3_h	GPA	EGS	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	941	
ZC504.4_ce	EGADDS	TS	GP	ED	TR	AA	SS	PN	LS	NG	ET	ES	VK	TM	IV	HD	DV	VE	SE	PAM	TP	--	SK	EG	TL	IV	--	772
NIK_m	EGADES	TS	GP	ED	TR	AA	SS	LN	LS	NG	ET	ES	VK	TM	IV	HD	DV	VE	SE	PAM	TP	--	SK	EG	TL	IV	--	901
ZC1_h	ETHD	GT	VA	VS	DI	PR	LI	PT	GA	PS	NE	QY	NV	GM	VG	TH	GL	ET	SH	AD	SF	SG	SI	SR	EG	TL	MIRE	907
ZC2_h	GPA	EGS	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	965	
ZC3_h	GPA	EGS	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	994	
ZC4_h	GPA	EGS	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	5	
ZC504.4_ce	EGADDS	TS	GP	ED	TR	AA	SS	PN	LS	NG	ET	ES	VK	TM	IV	HD	DV	VE	SE	PAM	TP	--	SK	EG	TL	IV	--	772
NIK_m	EGADES	TS	GP	ED	TR	AA	SS	LN	LS	NG	ET	ES	VK	TM	IV	HD	DV	VE	SE	PAM	TP	--	SK	EG	TL	IV	--	901
ZC1_h	ETHD	GT	VA	VS	DI	PR	LI	PT	GA	PS	NE	QY	NV	GM	VG	TH	GL	ET	SH	AD	SF	SG	SI	SR	EG	TL	MIRE	907
ZC2_h	GPA	EGS	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	965	
ZC3_h	GPA	EGS	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	994	
ZC4_h	GPA	EGS	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	5	
ZC504.4_ce	EGADDS	TS	GP	ED	TR	AA	SS	PN	LS	NG	ET	ES	VK	TM	IV	HD	DV	VE	SE	PAM	TP	--	SK	EG	TL	IV	--	772
NIK_m	EGADES	TS	GP	ED	TR	AA	SS	LN	LS	NG	ET	ES	VK	TM	IV	HD	DV	VE	SE	P								

### Fig. 3E

ZC504.4_ce	DQM	TV	LEG	Q	N	I	L	A	T	I	S	G	R	K	R	R	I	R	V	Y	L	S	W	L	R	Q	K	I	L	R	T	E	G	A	G	S	A	N	T	T	E	K	R	N	G	W	V	N	V	G	D	--	889								
NIK_m	QQ	MD	V	LEG	N	V	L	V	T	I	S	G	K	K	D	K	L	R	V	Y	L	S	W	L	R	N	K	I	L	H	N	D	P	E	V	--	--	--	--	--	--	--	--	--	--	--	--	--	--	1013											
ZC1_h	QQ	MD	V	LEG	N	V	L	V	T	I	S	G	K	K	D	K	L	R	V	Y	L	S	W	L	R	N	K	I	L	H	N	D	P	E	V	--	--	--	--	--	--	--	--	--	--	--	--	--	1019												
ZC2_h	QQ	MD	V	LEG	N	V	L	V	T	I	S	G	K	K	N	K	L	R	V	Y	L	S	W	L	R	N	R	I	L	H	N	D	P	E	V	--	--	--	--	--	--	--	--	--	--	--	--	--	1077												
ZC3_h	QQ	MD	V	LEG	N	L	I	T	I	S	G	K	R	N	K	L	R	V	Y	L	S	W	L	R	N	K	I	L	H	N	D	P	E	V	--	--	--	--	--	--	--	--	--	--	--	--	--	1106													
ZC4_h	R	Q	L	Q	V	L	E	P	L	N	L	I	T	I	S	G	H	K	N	R	L	R	V	Y	H	L	T	W	L	R	N	K	I	L	N	D	P	E	S	--	--	--	--	--	--	--	--	--	--	--	120										
ZC504.4_ce	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	944												
NIK_m	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	1068													
ZC1_h	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	1074													
ZC2_h	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	1132													
ZC3_h	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	1161													
ZC4_h	K	A	I	D	K	L	T	G	C	E	H	F	S	V	L	Q	H	E	T	T	Y	I	A	I	A	L	K	S	I	H	L	Y	A	W	A	P	K	S	F	D	E	S	T	A	I	K	V	E	P	T	L	D	H	K	P	V	T	V	--	180	
ZC504.4_ce	D	L	T	V	E	D	N	A	R	L	K	V	L	Y	G	S	T	G	F	H	A	I	D	L	D	S	A	A	V	Y	D	I	Y	T	P	A	Q	S	G	Q	T	T	I	P	H	C	I	V	V	L	P	N	S	N	G	M	Q	L	L	1004	
NIK_m	D	L	T	V	E	E	G	Q	R	L	K	V	I	Y	G	S	C	A	G	F	H	A	V	D	V	D	S	G	S	V	Y	D	I	Y	L	P	T	H	I	Q	C	S	I	K	P	H	A	I	I	L	P	N	T	D	G	M	E	L	L	1128	
ZC1_h	D	L	T	V	E	E	G	Q	R	L	K	V	I	Y	G	S	C	A	G	F	H	A	V	D	V	D	S	G	S	V	Y	D	I	Y	L	P	T	H	I	Q	C	S	I	K	P	H	A	I	I	L	P	N	T	D	G	M	E	L	L	1134	
ZC2_h	D	L	T	V	E	E	G	Q	R	L	K	V	I	F	G	S	H	T	G	F	H	V	I	D	V	D	S	G	S	V	Y	D	I	Y	T	P	S	H	I	Q	G	N	I	T	P	H	A	I	V	I	L	P	K	T	D	G	M	E	M	L	1192
ZC3_h	D	L	T	V	E	E	G	Q	R	L	K	V	I	Y	G	S	S	A	G	F	H	A	V	D	V	D	S	G	S	V	Y	D	I	Y	I	P	V	H	I	Q	S	I	T	P	H	A	I	I	F	L	P	N	T	D	G	M	E	M	L	1221	
ZC4_h	D	L	A	I	G	S	E	K	R	L	K	I	F	F	S	S	A	D	G	Y	H	L	I	D	A	E	S	E	V	M	S	D	V	T	L	P	K	N	P	L	E	I	I	P	Q	N	I	I	L	P	D	C	L	G	I	G	M	M	240		

Fig. 3F

ZC504.4\_ce L C Y D N E G V Y V N T Y G R I T K N V V L Q W G E M P S S V A Y I S T G Q I M G W G N K A I E I R S V I D T G H L D G V 1064  
 NIK\_m V C Y E D E G V Y V N T Y G R I T K D V V L Q W G E M P T S V A Y I R S N Q T I M G W G E K A I E I R S V E T G H L D G V 1188  
 ZC1\_h V C Y E D E G V Y V N T Y G R I T K D V V L Q W G E M P T S V A Y I R S N Q T I M G W G E K A I E I R S V E T G H L D G V 1194  
 ZC2\_h V C Y E D E G V Y V N T Y G R I T K D V V L Q W G E M P T S V A Y I H S N Q I M G W G E K A I E I R S V E T G H L D G V 1252  
 ZC3\_h L C Y E D E G V Y V N T Y G R I I K D V V L Q W G E M P T S V A Y I C S N Q I M G W G E K A I E I R S V E T G H L D G V 1281  
 ZC4\_h L T F N A E A L S V E A N E Q L F K K I L E M W K D I P S S I A F E C T D R T T G W G Q K A I E V R S L Q S R V L E S E 300

ZC504.4\_ce F M H K K A Q K L K F L C E R N D K V F F S S A K G G S C Q I Y F M T L N K P G L T N W 1109  
 NIK\_m F M H K R A Q R L K F L C G R N D K V F F S S V R S G G S S Q V Y F M T L G R T S L L S W 1233  
 ZC1\_h F M H K R A Q R L K F L C E R N D K V F F A S V R S G G S S Q V Y F M T L G R T S L L S W 1239  
 ZC2\_h F M H K R A Q R L K F L C E R N D K V F F A S V R S G G S S Q V F F M T L N R N S M M N W 1297  
 ZC3\_h F M H K R A Q R L K F L C E R N D K V F F A S V R S G G S S Q V Y F M T L N R I M N W 1326  
 ZC4\_h L K R R S I K K L R F L C T R G D K L F F T T S T L R N H H S R V Y F M T L G K L E E L Q S N Y D V 349

Fig. 3G

KHS1_h	5	LRPAADILRRNPQQDYELVQRVGS	GT	Y	GD	VY	KARNVHTGELAAVKIIKLEPGDDFSLIQQ	64
KHS2_h	1	MNPGFDLSRRNPQEDFELIQRIGSG	TY	GD	VY	KARNVNTGELAAIKVIKLEPGEDFAVVQQ	60	
KHS1_h	65	EIFMVKECKHCNIVAYFGSYLSREK	LW	IC	MEYCGG	SLQDIYHVTGPLSELQIAYVCRET	124	
KHS2_h	61	EIIMMKDCKHPNIVAYFGSYLRRDK	LW	IC	MEFCGG	SLQDIYHVTGPLSELQIAYVSRET	120	
KHS1_h	125	LQGLAYLHTKGKMH	RD	IK	GANILL	TDHGDVKLADFGVAAKITATIAKRKSF	184	
KHS2_h	121	LQGLYLYLSKGMHR	DI	K	GANILL	TDNGHVKLADFGVSAQITATIAKRKSF	180	
KHS1_h	185	EVA	AVEKNGGYNQLCDI	W	AVGITA	IELGELQPPMFDLHPMRALFLMSKSNFQPPKLKDKT	244	
KHS2_h	181	EVA	AVERKGGYNQLCDL	W	AVGITA	IELAELQPPMFDLHPMRALFLMTKSNFQPPKLKDKM	240	
KHS1_h	245	KWSSTFHN	FVKIA	L	T	KNPKKRPTAERLLTHTFVAQPGLSRALAVELL	304	
KHS2_h	241	KWSNSFHHFVKMA	L	T	KNPKKRPTAEKLLQHPFVTQH-L	TRSLAIELLDKVN	298	
KHS1_h	305	EADDDDFEPHAI	IRHT	IR	STNRNARAERTASE	INFDKLQFEPPLRKETEARD	361	
KHS2_h	299	DFDDDDPEPL	V	AVPHRIHSTSRNV	REEKTRSEIT	FGQVKFDPPLRKETEPHHELP	358	



**Fig. 4C**

SULU_ce	L I Q R T K N M V L E L D N F Q Y K K M R K L M Y L D E T E G K E G S E G N G A S D D L D F H G N E A N S I G R A G D S	360
SULU1_h	L I Q R T K D A V R E L D N L Q Y R K M K K I L F - - - - -	313
SULU3_m	L I Q R T K D A V R E L D N L Q Y R K M K K L L F - - - - -	309
SULU3_h	L I O R T K D A V R E L D N L O Y R K M K K L L F - - - - -	103

**Fig. 5A**



SULU\_ce ASSRSASLT SFRSMQSSGGAGLLVSTNTTGAMDNVHGSSGYGNGSSSTTSSARRRRPPIPS 420  
 SULU1\_h ----- QETRNGPPLNES 324  
 SULU3\_m ----- QEAHNGPAVEA 320  
 SULU3\_h ----- QEAHNGPAVEA 114

SULU\_ce QMLSSSTSTSGVG TMP SHG SVGASITAI AVNPTPSPSEPIPTSQPTSKSES S-SILETAHD 479  
 SULU1\_h QED EEDSEHG TSLNREMDSLG SNHSIPSM SVSTGSSQSSSVNSM QEVMD EESSSELVMMHDD 384  
 SULU3\_m QEEEEEEQDHGVGR TGT VNSVGVSNQSI PSMSISASSSQSSSVNSLPDASDDKS-ELDMMEGD 379  
 SULU3\_h QEEEEEEQDHGVGR TGT VNSVGVSNQSI PSMSISASSSQSSSVNSLPDVSDDKS-ELDMMEGD 173

SULU\_ce DPLDTSI ----- RAPVKKDLHMPHRAVKERIA TLQNHK FATLR SQRII 521  
 SULU1\_h ESTINS SS SVVHK KDHVFTRD EAGHGDP RPPTQSVQSQALHYRNRE RFATIKSASLV 444  
 SULU3\_m HTVMSN SS VIHLKPEEENYQE EGDPR TRASDPQSPQVSRHKSHYRNRE HFATIR TASLV 439  
 SULU3\_h HTVMSN SS VIHLKPEEENYRE EGDPR TRASDPQSPQVSRHKSHYRNRE HFATIR TASLV 233

SULU\_ce NQEQEEYTKENNM YE QMSKYKHLRQA HHKELQQFEERCALDREQLRVKMDREL EQLT TTY 581  
 SULU1\_h TRQIHEHEQ ENELREQMSGYKKRMRRRQHKKQLIAL ENKLLKAEMDEHRLKLQKEVET HANN S 504  
 SULU3\_m TRQM QEHEQDSELREQMSGYKKRMRRRQHKKQLMTLE NKLLKAEMDEHRLRLDKDLET QRNNF 499  
 SULU3\_h TRQM QEHEQDSELREQMSGYKKRMRRRQHKKQLMTLE NKLLKAEMDEHRLRLDKDLET CRNNF 293

SULU\_ce SK EKMRVRC SQNNELDKRK KDIEDG EKKMKKT KNSQNNQQQMKLYSAQQLKEYKYNKEAQK 641  
 SULU1\_h SIELEKLA KKQV AII EKEAKVAAADEKKFQQQII LAQQKKDL TTFLESQKKQYKICK EKIK 564  
 SULU3\_m AAEMEKL I KKHQAA MEKEAKVMANEEKKFQQQHIIQAQQKKELNS FLESQKREYKLRKEQLK 559  
 SULU3\_h AAEMEKL I KKHQAA MEKEAKVMSNEEKKFQQQHIIQAQQKKELNS FLESQKREYKLRKEQLK 353

Fig. 5B

SULU\_ce TRLSNM-PRSTYENAMKEVKADLNRVKDAREND FDEKLRRAEL EDEIVRYRQQQLSNLH 700  
 SULU1\_h EEMNEDHSTPKKEKQERISKHKENLQHTQAEEEEAHLLTQQRLLYYDKNCRFFFKRKIMIKRH 624  
 SULU3\_m EELNENQSTPKKEKQEWLSKQKENIQHFQAEEEEANLLRRQRQYLELECCRFFKRRMLLGRH 619  
 SULU3\_h EELNENQSTPKKEKQEWLSKQKENIQHFQAEEEEANLLRRQRQYLELECCRFFKRRMLLGRH 413

SULU\_ce QLEEQQLDDEVDVNVQERQMDTRHGLLSKQHEMTRDLEIQHLNELHAMKKRHL ETQHHEAESA 760  
 SULU1\_h EVEEQQNIREEELNKKRRTQKEMEHA MLIRHDESTR ELEYRQLHTLQKLRMDLIRLQHQT ETEL 684  
 SULU3\_m NLEQDLVREEELNKKRQTQKDLEHA MLIRQHESMQELEEFRLNNTIQKMRCELIRLQHQT ETEL 679  
 SULU3\_h NLEQDLVREEELNKKRQTQKDLEHA MLIRQHESMQELEEFRLNNTIQKMRCELIRLQHQT ETEL 473

SULU\_ce SQNEYTQRQQDELRLKKHAMQS RQQPRDLKIQEAQIRKQYRQVVVKTTQTRQFKLYLTQM VQV 820  
 SULU1\_h NQLEYNKKRRERELHRKKHVMGLRQQPKNLKAMEMQIKKKQFQDTCKVQTKQYKALKNHQLEV 744  
 SULU3\_m NQLEYNKKRRERELRRKKHVM EVRQQPKSLKSKELQIKKKQFQDTCKIQTRQYKALRNHLLET 739  
 SULU3\_h NQLEYNKKRRERELRRKKHVM EVRQQPKSLKSKELQIKKKQFQDTCKIQTRQYKALRNHLLET 533

SULU\_ce VPKDEQKELTSRLKQDQMVKVALLASQYYESQIKKMMVQDKTVKLESWQED EQRVLSEKLEK 880  
 SULU1\_h TPKNEHKTILKTLKDEQTRKLAIALAEQYEQSINEMMASQALRLDEAQEAECQALLQLQQ 804  
 SULU3\_m TPKNEHKA I 748  
 SULU3\_h TPKSEHKA VLRKLKEEQTRKLAIALAEQYDHSINEMLSTQALRLDEAQEAECQVLLKMQLLQQ 593

SULU\_ce ELEELIAYQKKTRATLLEEQIKKKERTALEERIGTRRAMLEQKIIEEEREQMGEMRLKKKEQI 940  
 SULU1\_h EMELLNAYQSKIKMQTEAQHERELQKLEQRVSLRRRAHLEQKIEEELAAALQKERSERIKNL 864  
 SULU3\_h ELELLNAYQSKIKMQAEAQHDRELRELLEQRVSLRRRAHLEQKIEEELMALLQNERTERIRSL 653

Fig. 5C



```
*****
1 MAFANFRRIILRLSTFEKRSREYEHVRRDLDPNDVWEIVGELGDGAFGKVYKAKNKETGA 60
GEK2_h 1 MAFANFRRIILRLSTFEKRSREYEHVRRDLDPNEVWEIVGELGDGAFGKVYKAKNKETGA 60

*****
61 LAAAKVIETKSEEELEDYIVEIEILATCDHPYIVKLLGAYYDGKWLWIMIEFCPGGAVDA 120
GEK2_h 61 LAAAKVIETKSEEELEDYIVEIEILATCDHPYIVKLLGAYYHDGKWLWIMIEFCPGGAVDA 120

*****
121 IMLELDRGLTEPQIQVVCQRQMLEALNFLHGKRIIHRDLKAGNVLMTLEGDIRLADFGVSA 180
GEK2_h 121 IMLELDRGLTEPQIQVVCQRQMLEALNFLHRSKRIIHRDLKAGNVLMTLEGDIRLADFGVSA 180

*****
181 KNLKTLQKRDSFIGTPYWMAPEVVMCETMKDAPYDYKADIWSLGI TLIEMAQIEPPHHEL 240
GEK2_h 181 KNLKTLQKRDSFIGTPYWMAPEVVMCETMKDTPYDYKADIWSLGI TLIEMAQIEPPHHEL 240

*****
241 NPMRVLLKIAKSDPPTLLTPSKWSVEFRDFLKI ALDKNPETRPSAAQLLQHPFVSRVTSN 300
GEK2_h 241 NPMRVLLKIAKSDPPTLLTPSKWSVEFRDFLKI ALDKNPETRPSAAQLLEHPFVSSITSN 300

*****
301 KALRELVAEAKAEVMEEIEDGREDEGEEDAVDA VPPLVNHTQDSANVTQPSLDSNKL LQD 360
GEK2_h 301 KALRELVAEAKAEVMEEIEDGREDEGEEDAVDA ASTLENHTQNSSEVSPPSLNADKPLEE 360
```



```

*****
720 ICDKERDCLSKKQELLRDREAALWEMEEHQLQERHQLVKQQLKDQYFLQRHDLRLRKHEKE 779
721 ICDKERECLMKKQELLRDREAALWEMEEHQLQERHQLVKQQLKDQYFLQRHELRLRKHEKE 780

*****
780 REQMQRYNQRMMEQLKVRQQQEKAARLPKIQSDGETRMAMYKKSLHINGAGSASEQREKI 839
781 REQMQRYNQRMIEQLKVRQQQEKAARLPKIQSEGKTRMAMYKKSLHINGGGSAAEQREKI 840

*****
840 KQFSQQEERQKAERLQQQKKHEHQMRDMVAQCESNMSELQQQLQNEKCYLLVEHETQKLK 899
841 KQFSQQEERQKSERLQQQKKHENQMRDMLAQCESNMSELQQQLQNEKCHLLVEHETQKLK 900

*****
900 ALDESHNQSLKE 911
901 ALDESHNQNLKE 912
```

Fig. 6C

PAK1_h	MSNNGLDIQDKPPAPP	MRNTSTMIGAGSKDAGTL	NHGS	KPLPPN	PPEEK	KKKDRFYRSIL	- 59
PAK65_h	MEETQQKSHLELLSA	- - - - -	- - - - -	NHSL	KPLPSV	PPEEK	KPRHKIISIFS - 40
PAK3_m	-MSDSLNEEKPPAPPLR	- - - - -	MNSNRDSSALNHSS	KPLPMA	PPEEK	NKKARLSIFPG	54
PAK1_h	PGDK	TNKKKEKERPEIS	LP	PSDFEHTIHVGFD	DA	VTGEFTGM	PEQWARLLQTSNITKS - - - 115
PAK65_h	GTEK	GSKKKEKERPEIS	PP	PSDFEHTIHVGFD	DT	VTGEFTGM	PEQWARLLQTSNITKL - - - 96
PAK3_m	GGDK	TNKKKEKERPEIS	LP	PSDFEHTIHVGFD	DA	VTGEFTGI	PEQWARLLQTSNITKL - - - 110
PAK4_h	- - - - -	MFRKKKKRPEIS	AP	QN	FQHRVHTS	FD	PK
							EGKFVGLPPQWQNI
							LDITLRRPK
							PVVDP
PAK1_h	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - 115
PAK65_h	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - 96
PAK3_m	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - 110
PAK4_h	SRITRVQLQPMKTVVRGS	AMPVDGYISGLLNDIQKLS	VISSNTLRGRSPT	SRRAQSLGL	116		
PAK1_h	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - 115
PAK65_h	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - 96
PAK3_m	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - 110
PAK4_h	LGDEHWATDPDMYLQSPQ	SERTDPHGLYLS	CNGGTPAGHKQMPWPEP	QSPRVLP	PNGLAAK	176	
PAK1_h	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - 127
PAK65_h	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - 108
PAK3_m	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - 122
PAK4_h	AQSLGPAEFQGASQRCLQL	GACLQSSPPGASPP	TG	TRHGMKA	AKHGS	FEARPQ	SCLVGS 236

Fig. 7A





PAK1_h	GDELWVVM EYLAGGSLTDVVV TETCMDEGQIAAVCRECLQAL	ESLHSNQVVIHRDIKSDN	IL	396
PAK65_h	GDEL[FVVM EYLAGR]SLTDVVV TETCMDEAQIAAVCRECLQAL	EFLLHANQVVIHRDIKSDN	VL	357
PAK3_m	GDELWVVM EYLAGGSLTDVVV TETCM DVGQIAAVCRECLQAL	DFLHSNQVVIHRDIKSDN	IL	394
PAK4_h	G[E]ELWV[L]MEFLQGGALTDIIVSQVRLNEEQIA[T]VCEAVLQAL	AYLHAQQGVVIHRDIKSDS	IL	533
PAK5_h	GDELWVVM EFLLEGGALTDIIVT[TR]MNEEQIAAVCLAVLQAL	SVLHAQQGVVIHRDIKSDS	IL	254

PAK1_h	LGM DGSVKLTDFGFC AQITPEQSKRSTMVGTPTYWMAPEVVTRKAYGPKVDIWSL	GIM AIE	456	
PAK65_h	LGM[E]GSVKLTDFGFC AQITPEQSKRSTMVGTPTYWMAPEVVTRKAYGPKVDIWSL	GIM AIE	417	
PAK3_m	LGM DGSVKLTDFGFC AQITPEQSKRSTMVGTPTYWMAPEVVTRKAYGPKVDIWSL	GIM AIE	454	
PAK4_h	L[T]LDGRVKLSDFGFC AQISKDVPKRKSLVGTPTYWMAPEVISRSLYATEVDIWSL	GIM VIE	593	
PAK5_h	L[THDGRVKLSDFGFC AQVSK[E]VPRRKSLVGTPTYWMAPELISR	LPYGP EVDIWSL	GIM VIE	314

PAK1_h	M[IE]EGEPYLNENPLRALYLIATNGTPELQNPEKLSAIFRDFLNRCLEMDV	EKRGS AKELL	516
PAK65_h	MVEGEPPYLNENPLRALYLIATNGTPELQNPEKLSPIIFRDFLNRCLEMDV	EKRGS AKELL	477
PAK3_m	MVEGEPPYLNENPLRALYLIATNGTPELQNPERLSAV[FH]DFLNRCL EMDV	DRRGS AKELL	514
PAK4_h	MVDGEPPYFSDSPVQAMKRLRDSPP[KLKN]SHKVSPIVLRDFLERMLVRDPQER	ATAQELL	653
PAK5_h	MVDGEPPY[FNE]P[LKAMKM]IRD[NL]P[PR]LKNLHKVSPSLKGF[LDR]LLVRDPAQRA	TAAELL	374

PAK1_h	QHQFLKI	AKPLSSLTPLIA	A	A	K	E	A	T	K	N	N	H	545											
PAK65_h	QHPFLKL	AKPLSSLTPLI	I	M	A	A	K	E	A	M	K	S	N	506										
PAK3_m	QHPFLKL	AKPLSSLTPLI	I	I	A	A	K	E	A	I	K	N	S	544										
PAK4_h	DHPFL	LQ	T	G	L	P	E	C	L	V	P	L	I	Q	L	Y	R	K	Q	T	S	T	C	681
PAK5_h	KHPFL	A	K	A	G	P	P	A	S	I	V	P	L	M	R	Q	N	R	T	R	398			

Fig. 7C

SEQ ID NO: 5 STLK2 human Nterm=1-21 kin=22-274  
Cterm=275-416

MAHSPVAVQVPGMQNNIADPEELFTKLERIGKGSFGEVFKGIDNRTQQVVAIKIIDLEEA  
EDEIEDIQQEITVLSQCDSSYVTKYYGSYLKGSKLWIIMEYLGSGSALDLLRAGPFDEFQ  
IATMLKEILKGLDYLHSEKKIHRDIKAANVLLSEQGDVKLADFGVAGQLTDTQIKRNTFV  
GTPFWMAPEVIQQSAYDSKADIWSLGITAIELAKGEPPNSDMHPMRVLFLIPKNNPPTLV  
GDFTKSFKEFIDACLNKDPSFRPTAKELLKHKFIVKNSKTSYLTTELIDRFKRWKAEGHS  
DDES DSEGSDSESTSRENNTHPEWSFTTVRKKPDPKKVQNGAEQDLVQTLSCLSMIITPA  
FAELKQQDENNASRNQAIEELEKSIABAEAAACPGITDKMVKKLIEKFQKCSADESP

SEQ ID NO: 6 STLK3 human Nterm=1-31 kin=32-308 Cterm=309-489  
(insert=327-352) tail=490-516

TAAPAPAAPAAPAPAPAPAPAAQAVGWPICRDAYELQEVI GSGATAVVQAALCKPRQERV  
AIKRINLEKCQTSMDLLKEIQAMSQC SHPNVVTYYTTSFVVKDELWLVMKLLSGGSMLDI  
IKYIVNRGEHKNGVLEEAIATILKEVLEGLDYLHRNGQIHRDLKAGNILLGEDGSVQIA  
DFGVSAFLATGGDVTRNKVRKTFVGT PCWMAPEVMEQVRGYDFKADMWSFGITAIELATG  
AAPYHKYPPMKVLM LTLQNDPPTLETGVEDKEMMKY GKSFRKLLSLCLQKDPSKRPTAA  
ELLKCKFFQKAKNREY LIEKLLTRTPDIAQRAKKVRRVPGSSGHLHKTEDGDWEWSDDEM  
DEKSEEGKA AFSQEKSRVKEENPEIAVSASTIPEQIQSLSVHDSQGPPNANEDYREASS  
CAVNLVLR LRNSRKELNDIRFEFTPGRDTADGVSQELFSAGLVDGHDVVIVAANLQKIVD  
DPKALKTLTFKLASGCDGSEIPDEVKLIGFAQLSVS

SEQ ID NO: 7 STLK4 human Nterm=absent, kin=1-178, Ctail=179-414,  
insert1=198-222, insert2=253-293

KSGVLDXSTIATILREVLEGLEYLHKXGQIHRDVKAGNILXGEDGSVQIADFGVSAFLAT  
GGDITRNKVRKTFVGT PCWMAPEVMEQVRGYDFKADIWSFGITAIELATGAAPYHKYPPM  
KVLMLTLQNDPPSLETGVQDKEM LKKY GKSFRKMISLCLQKDPEKRPTAAELLRHKFFQK  
AKNKEFLQEKT LQRAPTISERAKKVRVPGSSGRLHKTEDGGWEWSDDEFDEESEEGKAA  
ISQLRSPRVKESISNSELFP TTD PVGTLLQVPEQISAHLPQPAQGIATQPTQVSLPPTAE  
PAKTAQALSSGSGSQETKIPISLVLR LRNSKKELNDIRFEFTPGRDTAEGVSQELISAGL  
VDGRDLVIVAANLQKIVEEPQSNRSVTFKLASGVEGSDIPDDGKLIGFAQLSIS

SEQ ID NO: 8 STLK5 human Nterm=absent, kin=1-222(lacks N-term),  
Ctail=224-274

LICTHFMDGMNELAIAYILQGV LKALDYIHHMGYVHRSVKASHILISVDGKVYLSGLRSN  
LSMISHGQRQRVVHDFPKYSVKVLPWLSPEVLQQNLQGYDAKSDIYSVGITACELANGHV  
PFKDMPATQMLLEKLN GTVPCLLDTSTIPAEELTMSPSRSVANSGLSDSLTTSTPRPSNG  
DSPSHPHYHRTFSPHFHHFVEQCLQRNP DARPSASTLLNHSFFKQIKRRASEALPELLRPV

TPITNFEGSQSQDHSGLVTNLEELEVDDWEF

SEQ ID NO: 13 ZC1 human 1/5/98 Nterm=1-22 kin=23-289

coiled-coil=290-526 pro=527-640 B=641-896 Rab/Rac-BD=897-1239

MANDSPAKSLVDIDLSSLRDPAGIFELVEVVGNGTYGQVYKGRHVKTGQLAAIKVMDVTE  
DEEEEIKLEINMLKKYSHHRNIATYYGAFIKKSPPGHDDQLWLVMFEFCGAGSITDLVKNT  
KGNTLKEDWIAYISREILRGLAHLHIHHVIHRDIKGQNVLLTENA EVKLVD FGVSAQLDR  
TVGRRNTFIGTPYWMAPEVIACDENPDATYDYRSDLWSCGITAIEMAEGAPPLCDMHPMR  
ALFLIPRNPPPRLKSKKWSKKFFSFIEGCLVKNYMQRPSTEQLLKHPFIRDQPNERQVRI  
QLKDHIDRTRKKRGEKDETEYEYSGSEEEEEEEVPEQEGEPSSIVNVPGESTLRRDFLRQLQ  
QENKERSEALRRQQLLQEQQLREQEEYKRQLLAERQKRIEQQKEQRRRLEEQQRREREAR  
RQQEREQRRREQEKKRLEELERRRKEEEEERRRAEEEKRRVEREQEYIRRLQLEEEQRHLE  
VLQQQLLQEQAMLLECRWREMEEHRQAERLQRQLQQEQAYLLSLQHDHRRPHPQHSQQPP  
PPQQERSKPSFHAPEPKAHYEPADRAREVEDRFRKTNHSSPEAQSKQTGRVLEPPVPSRS  
ESFSNGNSESVHPALQRPAEPQVPVRTTSRSPVLSRRDSPLQGGSGQQNSQAGQRNSTSIE  
PRLLWERVEKLVPRPGSGSSSSGSSNSGSQPGSHPGSQSGSGERFRVRSSSKSEGSPSQR  
L ENAVKKPEDKKEVFRPLKPADLTALAKELRAVEDVRPPHKVTDYSSSSEESGTTDEEDDD  
VEQEGADESTSGPEDTRAASSLNLSNGETESVKTMIVHDDVESEPA MTPSKEGTLIVRRT  
QSASSTLQKHKSSSSFTPFIDPRLLQISPSSGTTVT SVVGFSCDGM RPEAIRQDPTRKGS  
VVNVNPTNTRPQSDTPEIRKYKKRFNSEILCAALWGVNLLVGTESGLMLLDRSGQGKVYP  
LINRRRFQQMDVLEGLNVLVLTISGKKDKLRVYYLSWLRNKHNDPEVEKKQGWTTVGD  
L EGC VHYKVVKYERIKFLVIALKSSVEVYAWAPKPYHKFMAFKSFGELVHKPLLVDLTVEE  
GQRLKVIYIGSCAGFHAVD VDSGSVYDIYLP THIQCSIKPHAI IILPNTDGMELLVCYED  
E G VYVNTYGRITKDVVLQWGEMPTSVAYIRSNQTMGWGEKAIEIRSVETGHL DGVFMHKRA  
QRLKFLCERN DKVFFASVRSGGSSQVYFMTLGRTSLLSW

SEQ ID NO: 14 ZC2 human Nterm=missing kin=1-255 coiled-coil=256-442  
pro=443-626 B=627-954 Rab/RacBD=955-1297

AFGEVYEGRHVKTGQLAAIKVMDVTGDEEEEIKQEINMLKKYSHHRNIATYYGAFIKKNP  
PGMDDQLWLVMFEFCGAGSVTDLIKNTKGNTLKEEWIAYICREILRGLSHLHQHKVIHRDI  
KGQNVLLTENA EVKLVD FGVSAQLDR TVGRRNTFIGTPYWMAPEVIACDENPDATYDFKS  
DLWSLGITAIEMAEGAPPLCDMHPMRALFLIPRN PAPRLKSKKWSKKFQSFIESCLVKNH  
SQRPATEQLMKHPFIRDQPNERQVRIQLKDHIDRTRKKRGEKDETEYEYSGSEEEEEEND  
SGEPSSILNLPRESTLRRDFLRQLANKERSEALRRQQLLEQQQRENEEHKRQLLAERQKR  
IEEQKEQRRRLEEQQRRREKELRKQQEREQRRHYEEQMRREEERRRAEHEQEYKRKQLEE  
Q RQAERLQRQLKQERDYLVS LQHQRQEQR PVEKKPLYHYKEGMSPSEKPAWAKEVEERSRL  
NRQSSPAMPHKVANRISDPNLPPRSESFSISGVQPARTPPMLRPVDPQIPHLVAVKSQGP  
ALTASQSVHEQPTKGLSGFQEALNVTSHRVEMPRQNSDPTSENPLPTRIEKFDRSSWLR

QEEDIPPKVPQRTTSSISPALARKNSPGNGSALGPRLGSQPIRASNPDLRRTEPILESPLQ  
 RTSSGSSSSSSSTPSSQPSQGGSQPGSQAGSSERTRVRANSKSEGSPVLPHEPAKVKEE  
 SRDITRPSRPASYKKAIDEDLTALAKELRELRIEETNRPMKKVTDYSSSSSEESSESEEE  
 EDGESETHDGTAVSDIPRLIPTGAPGSNEQYNVGMVGTHGLETSHADSFSGSISREGTL  
 MIRETSGEKKRSGHSDSNGFAGHINLPDLVQQSHSPAGTPTGLGRVSTHSQEMDSGTEY  
 GMGSSTKASFTPFVDPRVYQTSPTDEDEDEEESAAALFTGELLRQEQAALNEARKISVV  
 NVNPTNIRPHSDTPEIRKYKKRFNSEILCAALWGVNLLVGTENGLMLLDRSGQGKVYNLI  
 NRRRFQQMDVLEGLNVLVLTISGKKNKLRVYYLSWLRNRILHNDPEVEKKQGWITVGDLEG  
 CIHYKVVKYERIKFLVIALKNAVEIYAWAPKPYHKFMAFKSFADLQHKPLLVDLTVEEGQ  
 RLKVIFGSHTGFHVIDVDSGNSYDIYTPSHIQGNITPHAIVILPKTDGMEMLVCYEDEGV  
 YVNTYGRITKDVLQWGEEMPTSVAYIHSNQIMGWGEKAIEIRSVETGHLDGVMHKRAQR  
 LKFLCERNKDVFFASVRSGGSSQVFFMTLNRNSMMNW

SEQ ID NO: 15 ZC3 human kin=1-255 coiled-coil=256-476 pro=477-680  
 B=681-983 Rab/RacBD =984-1326

AFGEVYEGRHVKTGQLAAIKVMDVTEDEEEEIKQEINMLKKYSHHRNIATYYGAFIKKSP  
 PGNDQLWLVMFCGAGSVTDLVKNTKGNALKEDCIAYICREILRGLAHLHAHKVIHRDI  
 KGQNVLLTENAELVDFGVSAQLDRTVGRNRTFIGTPYWMAPVIAACDENPDATYDYRS  
 DIWSLGITAIEMAEGAPPLCDMHPMRALFLIPRNPPRLKSKKWSKKFIDFIDTCLIKTY  
 LSRPTEQLLKFPFIRDQPTERQVRIQLKDHIDRSRKKRGEKEETEYYSGSEEDDSHG  
 EEGEPSSIMNVPGESTLRREFLRLQQENKSNSEALKQQQQQLQQQQQRDPEAHIKHLLHQR  
 QRRIEEQKEERRRVEEQRRREREQRKLQEKEQRRLEDQMALRREEERRQAEREQEYIRH  
 RLEEEQRQLEILQQQLLQEQAALLLEYKRKQLEEQRQSERLQRQLQQEHAYLKSLLQQQQQ  
 QQLQKQQQQQLLPGDRKPLYHYGRGMNPADKPAWAREVEERTRMNKQQNSPLAKSKPGST  
 GPEPPIPQASPGPPGPLSQTTPMQRVPEQEGPHKSLVAHRVPLKPYAAPVPRSQSLQDQ  
 PTRNLAAFPASHDPDPAIPAPTATPSARGAVIRQNSDPTSEGGPSPNPPAWVRPDNEAP  
 PKVPQRTSSIATALNTSGAGGSRPAQAVRARPRSNSAWQIYLQRRRAERGTPKPPGPPAQP  
 PGPPNASSNPDLRRSDPGWERSDSVLPASHGHLPAAGSLERNRVGVSSKPDSSPVLSPGN  
 KAKPDDHRSRPGRPADFVLLKERTLDEAPRPPKKAMDYSSSSSEEVESSEDDEEEGEGGPA  
 EGSRDTPGGRDGDTSVSTMVVHDVEEITGTQPPYGGGTMMVVQRTPEEERNLLHADSNY  
 TNLPDVVQPSHSPTENSKGQSPPSKDGSGDYQSRGLVKAPGKSSFTMFVDLGIYQPGGSG  
 DSIPITALVGGEGTRLDQLQYDVRKGSVVNVNPTNTRAHSETPEIRKYKKRFNSEILCAA  
 LWGVNLLVGTENGLMLLDRSGQGKVYGLIGRRRFQQMDVLEGLNLLITISGKRKNKLRVYY  
 LSWLRNKILHNDPEVEKKQGWTTVGDMEGCGHYRVVKYERIKFLVIALKSSVEVYAWAPK  
 PYHKFMAFKSFADLPHRPLLVDLTVEEGQRLKVIYGSAGFHAVDSDGNSYDIYIPVHI  
 QSQITPHAIIFLPNTDGMEMLLCYEDEGVYVNTYGRIIKDVVLQWGEEMPTSVAYICSNQI  
 MGWGEKAIEIRSVETGHLDGVMHKRAQRKFLCERNKDVFFASVRSGGSSQVYFMTLNR  
 NRIMNW

Title: NUCLEIC ACIDS ENCODING  
 PAK5 POLYPEPTIDES AND  
 METHODS OF USE THEREOF  
 Inventor(s): Gregory PLOWMAN et al.  
 DOCKET NO.: 034536-1034

**Fig. 8C**  
 28/76

SEQ ID NO: 16 ZC4 human Nterm kin coiled-coil pro B=missing  
Rab/RacBD=1-349

NVNPLYVSPACKKPLIHMYEKEFTSEICCGSLWGVNLLLGTRSNNLYLMDRSGKADITKLI  
RRRPFRQIQVLEPLNLLITISGHKNRLRVYHLTWLRNKILNNDPESKRRQEEMLKTEEAC  
KAIDKLTGCEHFSVLQHEETTYIAIALKSSIHLYAWAPKSFDESTAIKVFP TLDHKPVTV  
DLAIGSEKRLKIFFSSADGYHLIDAESEVMSDVTLPKNPLEIIIPQNIIILPDCLGIGMM  
LTFNAEALSVEANEQLFKKILEMWKDIPSSIAFECTQRTTGWGQKAIEVRSLQSRVLESE  
LKRRSIKKLRFLCTRGDKLFFTSTLRNHHSRVYFMTLGKLEELQSNDY

SEQ ID NO: 18 KHS2 human Nterm=1-13 kin=14-273 A=274-346  
Pro=347-534 RabBD =535-894

MNPGFDLSRRNPQEDFELIQRIGSGTYGDVYKARNVNTGELAAIKVIKLEPGEDFAVVQQ  
EIIMMKDCKHPNIVAYFGSYLRRDKLWICMEFCGGGSLQDIYHVTGPLSELQIAYVSRET  
LQGLYYLHSGKGMHRDIKGANILLTDNGHVKLADFGVSAQITATIAKRKSFITPYWMA  
EVAVERKGGYNQLCDLWAVGITAEI LAELQPPMFDLHPMRALFLMTKSNFQPPKLKDKM  
KWSNSFHVFVKMALTKNPKKRPTAEKLLQHPFVTQHLTRSLAIELLDKVNNDHSTYHDF  
DDDDPEPLVAVPHRIHSTSRNVREEKTRSEITFGQVKFDPPLRKETEPHHELPDSDGFLD  
SSEIYYTARSNDLQLEYGQGHQGGYFLGANKSLLKSVEEELHQRGHVAHLEDDEGDD  
ESKHSTLKAKIPPLPKPKSIFIPQEMHSTEDENQGTIKRCMSGSPAKPSQVPPRPPP  
PRLPPHKPVALGNGMSSFQLNGERDGS LCQQQNEHRGTNLSRKEKKDVPKPISNGLPPTP  
KVHMGACFSKVFNGCPLKIHCASSWINPDTRDQYLIFGAEEGIYTLNLNELHETSMEQLF  
PRRCTWLYVMNNCLLSISGKASQLYSHNLPGLFDYARQMQLPVAIPAHKLPDRILPRKF  
SVSAKIPETKWCQKCCVVRNPYTGHKYL CGALQTSIVLLEWVEPMQKFMLIKHIDFPIPC  
PLRMFEMLVVPEQEYPLVCVGVSRGRDFNQVVRFETVNPNSTSSWFTESDTPQTNVTHVT  
QLERDTILVCLDCCIKIVNLQGR LKSSRKLSSSELT FDFQIESIVCLQDSVLAFWKHGMQG  
RSFRSNEVTQEISDSTRIFRLLGSDRVVVLESRPTDNPTANSNLYILAGHENSY

SEQ ID NO: 22 SULU1 human N=1-21 kin=22-277 A=278-427  
coiled-coil1=428-637 B=638-751 coiled-coil2=752-898

MRKGV LKDPEIDDLFYKDDPEELF IGLHEIGHGSFGAVYFATNAHTNEVVAIKKMSYSGK  
QTHEKWQDILKEVKFLRQLKHPNTIEYKGCYLKEHTAWLVMEYCLGSASDLLLVHKKPLQ  
EVEIAAITHGALHGLAYLHSHALHRDIKAGNILLTEPGQVKLADFGSASMASPANSFVG  
TPYWMAPEVILAMDEGQYDGKVDIWSLGITCIELAERKPPLFNMNAMSALYHIAQNDSP  
LQSNEWTDSFRRFVDYCLQKIPQERPTSAELLRHDFVRRDRPLRVLIDLIQRTKDAVREL  
DNLQYRKMKKILFQETRNGPLNESQEDEEDSEHGTS LNREMDSLGSNHSIPSM SVSTGSQ  
SSSVNSMQEVMDSSSELVMMHDDDESTINSSSSSVVHKKDHVFTRDEAGHGDPRPEPRPTQ  
SVQSQUALHYRNRERFATIKSASLVTRQIHEHEQENELREQMSGYKRMRRQHQQQLIALEN  
KLKAEMDEHRLKLQKEVETHANNSSIELEKLAKKQVAIIEKEAKVAAADEKKFQQQILAQ

Title: NUCLEIC ACIDS ENCODING  
PAK5 POLYPEPTIDES AND  
METHODS OF USE THEREOF  
Inventor(s): Gregory PLOWMAN et al.  
DOCKET NO.: 034536-1034

**Fig. 8D**  
29/76

QKKDLTTFLESQKKQYKICKKEIKKEEMNEDHSTPKKEKQERISKHKENLQHTQAEAAAHL  
LTQQRLLYYDKNCRFFKRRKIMIKRHEVEQQNIREELNKKRTQKEMEHAMLRHDESTRELE  
YRQLHTLQKLRLDLRLQHQTELENQLEYNKRRELERLHRKHVMGLRQPKNLKAMEMQIK  
KQFQDTCKVQTKQYKALKNHQLEVTPEKNEHKTILKTLKDEQTRKLAILEAQYEQSINEMM  
ASQALRLDEAQEAECQALRLQLQEQEMELLNAYQSKIKMQTEAQHERELQKLEQRVSLRRA  
HLEQKIEEELAALQKERSERIKNLLERQEREIETFDMESLRMGFGNLVTLDFPKEDYR

SEQ ID NO: 23 SULU3 human Nterm=missing kin partial=1-66 A=67-215  
coiled-coil1=216-425 B=426-539 coiled-coil2=540-786 Ctail=687-786  
IELAERKPPLFNMNAMSALYHIAQNESPTLQSNEWSDYFRNFVDSCLQKIPQDRPTSEEL  
LKHIFVLRERPETVLIDLIQRTKDAVRELDNLQYRKMKKLLFQEAHNGPAVEAQEEEEEQ  
DHGVGRTGTVNSVGSNQSISSMSISASSQSSSVNSLPDVSDDKSELDMMEGDHTVMSNSS  
VIHLKPEEENYREEGDPRTASDPQSPQVSRHKSHYRNREHFATIRTASLVTRQMGEHE  
QDSELREQMSGYKRMRRQHQQKQMTLENKLKAEMDEHRLRLDKDLETQRNNFAAEMEKL  
KKHQAAMEKEAKVMSNEEKKFQQHIQAQQKKELNSFLESQKREYKLRKEQLKEELNENQS  
TPKKEKQEWLSKQKENIQHFQAEAAANLLRRQRQYLELECRRFKRRMMLLGRHNLEQDLVR  
EELNKRQTQKDLEHAMLLRQHESMQELEFRHLNTIQKMRCELIRLQHQTELTNQLEYNKR  
RERELRRKHVMEVRQQPKSLKSKELQIKKQFQDTCKIQTRQYKALRNHLLLETPKSEHKA  
VLKRLKEEQTRKLAILEAQYDHSINEMLSTQALRLDEAQEAECQVLKMLQEQELELLNAY  
QSKIKMQAEAQHDRELRELEQRVSLRRALLEQKIEEEMLALQNERTERIRSLLEQAREI  
EAFDSESMRLGFSNMVLSNLSPEAFSHSYPGASGWSHNPTGGPGPHWGHPMGGPPQAWGH  
PMQGGPQPWGHPSGPMQGVPRGSSMGVRNSPQALRRRTASGGRTAQGMSRSTSVTSQISNG  
SHMSYT

SEQ ID NO: 24 SULU3 murine Nterm=1-25 kin=26-273 A=274-422  
cc1=423-632 B=633-748 cc2=missing  
MPSTNRAGSLKDPEIAELFFKEDPEKLFTDLREIGHGSFGAVYFARDVRTNEVVAIKKMS  
YSGKQSTEKWQDIIKEVKFLQRIKHPNSIEYKGCYLREHTAWLVMYCLGSASDLLEVHK  
KPLQEVEIAAITHGALQGLAYLHSHTMIHRDIKAGNILLTEPGQVKLADFGSASMSPAN  
SFVGTPYWMAPEVILAMDEGQYDGVVWSLGITCIELAERKPPLFNMNAMSALYHIAQN  
ESPTLQSNMNDSCCLQKIPQDRPTSEELLKHMFLRERPETVLIDLIQRTKDAVRELDNLQ  
YRKMKKLLFQEAHNGPAVEAQEEEEEQDHGVGRTGTVNSVGSNQSISSMSISASSQSSSV  
NSLPDASDDKSELDMMEGDHTVMSNSSVIHLKPEEENYQEEGDPRTASDPQSPQVSRH  
KSHYRNREHFATIRTASLVTRQMGEHEQDSELREQMSGYKRMRRQHQQKQMTLENKLKAE  
MDEHRLRLDKDLETQRNNFAAEMEKLKKHQAAMEKEAKVMAEKKFQQHIQAQQKKEL  
NSFLESQKREYKLRKEQLKEELNENQSTPKKEKQEWLSKQKENIQHFQAEAAANLLRRQR  
QYLELECRRFKRRMMLLGRHNLEQDLVREELNKRQTQKDLEHAMLLRQHESMQELEFRHLN  
TIQKMRCELIRLQHQTELTNQLEYNKRRELERLRRKHVMEVRQQPKSLKSKELQIKKQFQD

TCKIQTRQYKALRNHLLLETPKNEHKAI

SEQ ID NO: 26 GEK2 human N=1-33 kin=34-294 A=295-337 B=338-472 215  
coiled-coil1=473-724 215 coiled-coil2=725-912

MAFANFRRLRLSTFEKRKSREYEHVRRDLDPNEVWEIVGELGDGAFGKVYKAKNKETGA  
LAAAKVIETKSEEELEDYIVEIEILATCDHPYIVKLLGAYYHDGKLWIMIEFCPPGGAVDA  
IMLELDRGLTEPQIQVVCQRMLEALNFLHSKRRIHRDLKAGNVLMTLEGDIRLADFGVSA  
KNLCTLQKRDSFIGTPYWMAPEVVMCETMKDTPYDYKADIWSLGITLIEMAQIEPPHHEL  
NPMRVLLKIAKSDPPTLLTPSKWSVEFRDFLKIALDKNPETRPSAAQLLEHPFVSSITSN  
KALRELVAEAKAEVMEEIEDGRDEGEEEDAVDAASTLENHTQNSSEVSPPSLNADKPLEE  
SPSTPLAPSQSQDSVNEPCSQPSGDRSLQTTSPPVVAPGNENGLAVPVPLRKS RVPVSM DA  
RIQVAQEKQVAEQGGDLSPAANRSQKASQSRPNSSALETLGGEKLANGSLEPPAQAAPGP  
SKRSDSCSSLCTSESMDYGTNLSTDLSLNKEMGSLSIKDPKLYKKTLKRTRKFVVDGVEV  
SITTSKIISEDEKKDEEMRFLRRQELRELRLQLKEEHRNQTQLSNKHELQLEQMHRFEQ  
EINAKKKFFDTELENLERQQKQVEKMEQDHAVRRREEARRIRLEQDRDYTRFQEQLKLM  
KKEVKNEVEKLPRQQRKESMKQKMEEHTQKKQLLDRDFVAKQKEDLELAMKRLTTDNRR  
ICDKERECLMKKQELLRDREAALWEMEEHQLQERHQLVKQQLKDQYFLQRHELLRKHEKE  
REQMQRYNQRMIEQLKVRQQQEKARLPKIQRSEGKTRMAMYKKS LHINGGGSAAEQREKI  
KQFSQQEEKRQKSERLQQQQKHENQMRDMLAQCESNMSELQQLQNEKCHLLVEHETQK LK  
ALDESHNQN LKE

SEQ ID NO: 29 PAK4 human Rac=1-51 A=52-224 Nterm=225-393  
kin=394-658 Ctail=659-681 residues 13-23

(SAPQNFQHRVH)= Cdc42 /Rac-binding motif

MFRKKKKKRPEISAPQNFQHRVHTSFDPKEGKFVGLPPQWQNILDTLRRPKPVVDPSRIT  
RVQLQPMKTVVRGSAMPVDGYISGLLNDIQKLSVISSNTLRGRSPTSRRRAQSLGLLGDE  
HWATDPD MYLQSPQSERTDPHGLYLSCNGGTPAGHKQMPWPEPQSPRVLPNGLAAKAQSL  
GPAEFQGASQRCLQLGACLQSSPPGASPTGTNRHGMKAAKHGSEEARPQSCLVGSATGR  
PGGEGSPSPKTRESSLKRRFLFRSMFLSTAATAPPSSSKPGPPPQSKPNSSFRPPQKDNPP  
SLVAKAQSLPSDQPVGTFSPLTTSDTSSPQKSLRTAPATGQLPGRSSPAGSPRTWHAQIS  
TSNLYLPQDPTVAKGALAGEDTG VVTHEQFKAALRMVVDQGDPRLLLLDSYVKIGEGSTGI  
VCLAREKHSGRQVAVKMMDLRKQQRRELLFNEVVIMRDYQHFN VVEMYKSYLVGEELWVL  
MEFLQGGALTDIVSQVRLNEEQIATVCEAVLQALAYLHAQGV IHRDIKSDSILLTLDGRV  
KLSDFGFC AQISKDVPKRKSLVGTPYWMAPEVISRSLYATEVDIWSLGIMVIEMVDGEP  
YFSDSPVQAMKRLRDSPPPKLKNSHKVSPVLRDFLERMLVRDPQERATAQELLDHPFL LQ  
TGLPECLVPLIQLYRKQTSTC

SEQ ID NO: 30 PAK5 human Rac A=missing Nterm partial=1-114  
kin=115-379 Ctail=380-398

ASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVAPNGPSAGGLAIPQSSSSSRPPTRA  
RGAPSPGVLGPHASEPQLAPPACTPAAPAVPGPPGPRSPQREPQRVSHEQFRAALQLVVD  
PGDPRS YLDNFIKIGEGSTGIVCIATVRSSGKLVAVKKMDLRKQQRRELLFNEVVIMRDY  
QHENVVEMYNSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAAVCLAVLQALSVLHA  
QGV IHRDIKSDSILLTHDGRVKLSDFGFCAQVSKEVPRRKSLVGTPYWMAPELISRLPYG  
PEVDIWSLGIMVIEMVDGEPPYFNEPPLKAMKMIRDNLPPRLKNLHKVSPSLKGFLDRLL  
VRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR

**Fig. 8G**



SEQ ID NO: 1 STLK2 HUMAN

TAACAGCCCACCTCCTAGCCCCGGGCTACGCGCCGCCAGCCCAGTAACCCCACCTTTTGTG  
TGTCCTCCCAGGCCCGGATCGAAAAGCCTGGGAGGGCCGCCGAACCTACCCCGGAGGGAG  
GAGCCAGTCCGAACCCAAGGCGCCACCGCCGCAGAAGCGGAGCGAGGCAGCATTTCGCCTC  
CATGGCCCACTCGCCGGTGGCTGTCCAAGTGCCTGGGATGCAGAATAACATAGCTGATCC  
AGAAGAACTGTTTACAAAATTAGAGCGCATTGGGAAAGGCTCATTTGGGGAAGTTTTCAA  
AGGAATTGATAACCGTACCCAGCAAGTCGTTGCTATTAAAATCATAGACCTTGAGGAAGC  
CGAAGATGAAATAGAAGACATTCAGCAAGAAATAACTGTCTTGAGTCAATGTGACAGCTC  
ATATGTAACAAAATACTATGGGTCATATTTAAAGGGGTCTAAATTATGGATAATAATGGA  
ATACCTGGGCGGTGGTTCAGCACTGGATCTTCTTCGAGCTGGTCCATTTGATGAGTTCCA  
GATTGCTACCATGCTAAAGGAAATTTTAAAAGGTCTGGACTATCTGCATTCAGAAAAGAA  
AATTCACCGAGACATAAAAGCTGCCAATGTCTTGCTCTCAGAACAAGGAGATGTTAAACT  
TGCTGATTTTGGAGTTGCTGGTCAGCTGACAGATACACAGATTAAAAGAAATACCTTTGT  
GGGAACTCCATTTTGGATGGCTCCTGAAGTTATTCAACAGTCAGCTTATGACTCAAAAGC  
TGACATTTGGTCATTGGGAATTACTGCTATTGAACTAGCCAAGGGAGAGCCACCTAACTC  
CGATATGCATCCAATGAGAGTTCTGTTTTCTTATTCCCAAAAACAATCCTCCAACCTCTTGT  
TGGAGACTTTACTAAGTCTTTTAAGGAGTTTATTGATGCTTGCCTGAACAAAGATCCATC  
ATTTGCTCCTACAGCAAAAGAACTTCTGAAACACAAATTCATTGTAAAAAATTCAAAGAA  
GACTTCTTATCTGACTGAACTGATAGATCGTTTTAAGAGATGGAAGGCAGAAGGACACAG  
TGATGATGAATCTGATTCCGAGGGCTCTGATTCGGAATCTACCAGCAGGGAAAACAATAC  
TCATCCTGAATGGAGCTTTACCACCGTACGAAAGAAGCCTGATCCAAAGAAAGTACAGAA  
TGGGGCAGAGCAAGATCTTGTGCAAACCTGAGTTGTTTGTCTATGATAATCACACCTGC  
ATTTGCTGAACTTAAACAGCAGGACGAGAATAACGCTAGCAGGAATCAGGCGATTGAAGA  
ACTCGAGAAAAGTATTGCTGTGGCTGAAGCCGCCTGTCCCGGCATCACAGATAAAATGGT  
GAAGAACTAATTGAAAAATTTCAAAGTGTTTACGACAGCAATCCCCCTAAGAACTTA  
TTATTGGCTTCTGTTTTCATATGGACCCAGAGAGCCCCACCAAACCTACGTCAAGATTAAC  
AATGCTTAACCCATGAGCTCCATGTGCCTTTTGGATCTTTGCAACACTGAAGATTTGGAA  
GAAGCTATTAACTATTTTGTGATGGCGTTTATCATTTTATATTTTGAAAGGATTATTTT  
GTAAGGAATAACTTTTAATACTATAGTTTACCTGTATTCTAGTAAATGTTGAGACACCG  
TTTTGCTTTTAAGTATCCCTATTTCTTAAGTTACGAGGATGAATACCTTTTACATTTTGA  
TCTTTAGTTGACTCTACAGTCATGAAACATACAGGTCTTTCAAAGTCATTCTCAATATTC  
AGCTTTTGTAAATTATCAAGCTTCAAAAAGCTTTTTTTTAAAAAATAACATGCATATT  
CTAAAAATGACTATTGGTGGGGAGGTGTAAATAAGTCATACCTTCTTAAAACAGAAAATT  
TAAGTAAAGTCTTTTAAATGAAACCTGTAAAAGTATTGACTCTTCTACCAAGTTGGTATG  
ATATTCCAGGCAGCTCAATGATTATCACATTTGAGACCCTGTGTTTGAAGCATTTACAGG  
CAATGTACAGCAACAGAGGTACCTCTTGGTGTATAGTATTTACATTCTCTTTTAGGTAGA  
AGAGGCAATTTTACCCTTATTTTACATGGTTAGAAATTTAAAGCAAGATCATTTACCCAA

GGATAGGTGTTTGGTAATGTTGAAGGAGTTAGTCTGGCTTCATGTTTTACATCTTCAACT  
 AAAATCCCATACTATCTGCTTGGATTTGGAGAGCCAAAAATAAAGCTGATTGTCATGTG  
 ATTAAATATCTGATCAACAGGTATGAATATAACTTAAATCAGCATATTTTTGCCATGGTA  
 ATAAATTGTCCTATAAACTATTTATATATTTTTGTTCTTCATAATTATCACTAATAAGCA  
 TCAGTTTGTGTTTTTAAAGGATATTTAAGTGAGCATTTTCTAGTTCATATGAAAATAA  
 CCATAGTACAGGATGATTTCTGTCCACACAAAGGTTAAATTAGATTGCACAGTTAATTTT  
 CACTTATATTTATGGTACTATTATGTGGGTGATGCCTTTTTCTTTTAAGCCCAGTACATA  
 TATTATGCCTGCCTAAGTTCTGAACTGGGGCTGTATTTAGTAGTTGTAGAATTATTGAT  
 ATTTAGTTTTTGATAGCTAATGTTTAATTGTTTGGATCTGCACAGTTTGGTTTTTGCACAA  
 AAGTCATTTAAAAAAATCTGAGTAATTGTCAAATATTTAAAAGAAAGATATTCTTCCTGTA  
 AGGAATACAGTTTTTAGTCAAAGTGCCATTACATCCTCTTTTAAATTTACATAATACAG  
 ATACTTGAGAAAGTTGTTGTGGTGTTGTATGCCAAGAAAATTCTTTTTATTGGTGCCTAT  
 ATTGTAACAATTATTTTTAATGCATTGTATTTGAAGTAACGGTTCAGTTAAATTTTTCA  
 CCTGCTGTGTAAC TGAAACACAATTACAGTTTATAATCATCTGTAGAAGTCTGGAGATAA  
 TTTTGCAACTCATGTTATGGGTTAAATGAATATTTTTGTAAAAGTAAAAGCAACAAATTT  
 ATAAATTGATTATTTGAAACTTTACAACACAATTGCATCCCAAATACAAATTGTATTGCT  
 TATTCATTATAGCTATTCGTCCTGTAATCTGTTTCTAGGTGAAGCATACTCCAGTGTTTT  
 AGGGGTTTTGAAAATAAATATTTAAATTTACAGTCAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 2 STLK3 HUMAN

GACAGCAGCGCCGGCCCCGGCAGCTCCCGCGGCCCCGGCCCCGGCCCCGGCCCCGGCCCC  
 GGCGGCACAGGCTGTGCGCTGGCCCATCTGCAGGGACGCGTACGAGCTGCAGGAGGTTAT  
 CGGCAGTGGAGCTACTGCTGTGGTTCAGGCAGCCCTATGCAAACCCAGGCAAGAACGTGT  
 AGCAATAAAACGGATCAACTTGGA AAAATGCCAGACCAGTATGGATGAACTATTTAAAGA  
 AATTCAAGCCATGAGTCAGTGCAGCCATCCCAACGTAGTGACCTATTACACCTCTTTTGT  
 GGTCAAAGATGAACTTTGGCTGGTCATGAAATTACTAAGTGGAGGTTCAATGTTGGATAT  
 CATAAAATACATTGTCAACCGAGGAGAACACAAGAATGGAGTTCTGGAAGAGGCAATAAT  
 AGCAACAATTCTTAAAGAGGTTTTTGAAGGCTTAGACTATCTACACAGAAACGGTCAGAT  
 TCACAGGGATTTGAAAGCTGGTAATATTCTTCTGGGTGAGGATGGTTCAGTACAAATAGC  
 AGATTTTGGGGTAAGTGC GTTCCTAGCAACAGGGGGTGATGTTACCCGAAATAAAGTAAG  
 AAAAACATTCGTTGGCACCCCATGTTGGATGGCTCCTGAAGTCATGGAACAGGTGAGAGG  
 CTATGACTTCAAGGCTGACATGTGGAGTTTTTGAATAACTGCCATTGAATTAGCAACAGG  
 AGCAGCGCCTTATCACAATATCCTCCCATGAAAGTGTTAATGTTGACTTTGCAAAATGA  
 TCCACCCACTTTGGAACAGGGGTAGAGGATAAAGAAATGATGAAAAGGTACGGCAAGTC  
 CTTTAGAAAATTACTTTCACTGTGTCTTCAGAAAGATCCTTCCAAAAGGCCACAGCAGC  
 AGAACTTTTAAATGCAAATTCTTCCAGAAAGCCAAGAACAGAGAGTACCTGATTGAGAA  
 GCTGCTTACAAGAACACCAGACATAGCCCAAAGAGCCAAAAAGGTAAGAAGAGTTCCTGG

GTCAAGTGGTCACCTTCATAAAACCGAAGACGGGGACTGGGAGTGGAGTGACGACGAGAT  
 GGATGAGAAGAGCGAAGAAGGGAAAGCAGCTTTTTCTCAGGAAAAGTCACGAAGAGTAA  
 AGAAGAAAATCCAGAGATTGCAGTGAGTGCCAGCACCATCCCCGAACAAATACAGTCCCT  
 CTCTGTGCACGACTCTCAGGGCCCCACCCAATGCTAATGAAGACTACAGAGAAGCTTCTTC  
 TTGTGCCGTGAACCTCGTTTTGAGATTAAGAACTCCAGAAAGGAACTTAATGACATACG  
 ATTTGAGTTTACTCCAGGAAGAGATACAGCAGATGGTGTATCTCAGGAGCTCTTCTCTGC  
 TGGCTTGGTGGATGGTCACGATGTAGTTATAGTGGCTGCTAATTTACAGAAGATTGTAGA  
 TGATCCCAAAGCTTTAAAAACATTGACATTTAAGTTGGCTTCTGGCTGTGATGGGTCGGA  
 GATTCTGATGAAGTGAAGCTGATTGGGTTTGCTCAGTTGAGTGTGAGCTGATGTATGTC  
 CCTTGATGTCACCCTGATCTGTCATGCCCCACCGCCACCCCTACTCCCTTCAACCCTCCC  
 TCTTTCTGCCCCATTTCTCTCCACCCCTCACTCCCATTTCTAGCAAAATCAGAAGATTG  
 TGAAGAGGGCCGGCTTCAACAAAATGGGATAAAAAAATAATTTTTTAAACTTTACAACACT  
 CCGAGTTCTGCTTTATTCTCTAGCAATCCACAGTACAAGAACAAGCAAATGCCACAGCTG  
 CACGACTGTTGCTCATTTTTTCCAAAAGCTATTTAATATTCTTAGCAATCAATTTGGATAT  
 CCCTTAAGTGAAAAGAATCTGAAATACACTCAGGTGGTCTTATTTATTGGCAACAAAAGG  
 AATTTTCTATCCAGAAGCCTATTTCTCCTTTTATTGTTGTTATTTCTGTTATAATACTTT  
 AATTGTACATCTGACAATACTGCCTCTTTTATGTTGTATTTAGAAATTAATATACTTATA  
 AAATTAAGATTTATTAGCCAAACTTGAATTCTAGTTTTAAACTGACTGTGAATTTTATT  
 TTTCATATATTTATGCATTACACACCTTAGCTATAAGAAAAAAGGGTTTTGATTATATG  
 CTTCTTGCAGTTAATCTCGTTATTTAAACAAAAAGTTTTGGGTCTATCTTTGGAGTATTT  
 GTAACCTCTAAATTTTGAATGACTGAATTAGGAATTTGGATGCTTATTCTTTTAGTCTG  
 TTTGCCTAAAAACCAATTTACAATCTGACTGTCTCTTGGGAGAGGGAGGTGCCTTGCAAA  
 CTTTCACATTAAGAATGTGCCTGAGGCTGCTTTACTCTGGAATAGTCTCAGATCTAAAT  
 TTCCTCTATATAAGGTGGCATAATGTTAAGTTTTGCTTCATTGGACCGTTTAGAATGCTAT  
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Title: NUCLEIC ACIDS ENCODING  
 PAK5 POLYPEPTIDES AND  
 METHODS OF USE THEREOF  
 Inventor(s): Gregory PLOWMAN et al.  
 DOCKET NO.: 034536-1034

**Fig. 9C**  
 35/76

T N T T G G A G A A G A T G G C T C A G T A C A G A T T T C A G A C T T T G G G G T T A G T G C T T T T T T A G C A A C  
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 GTCATCTTGCCTAAAACAGATGGAATGGAAATGCTTGTGTTGCTATGAGGATGAGGGGGTG  
 TATGTAAACACCTATGGCCGGATAACTAAGGATGTGGTGCTCCAATGGGGAGAAATGCC  
 ACGTCTGTGGCCTACATTCAATCCAATCAGATAATGGGCTGGGGCGAGAAAGCTATTGAG  
 ATCCGGTCAGTGGAAACAGGACATTTGGATGGAGTATTTATGCATAAGCGAGCTCAAAGG  
 TTAAGTTTCTATGTGAAAGAAATGATAAGGTATTTTTTGCATCCGTGCGATCTGGAGGA  
 AGTAGCCAAGTGTTTTTTCATGACCCTCAACAGAAATTCATGATACTGGTAACAGAAG  
 AGCACTTGGCACTTATCTTCATGGCGTTATTTCTAATTTAAAGAACATAACTCATGTGG  
 ACTTATGCCAGTCTAGAGGCAGAATCAGAAGGCTTGGTTGAACATATCGCTTTCCCTTTT  
 TCCTCTCCCTCCGCCCCCTCCAGTACAGTCCATCT

Title: NUCLEIC ACIDS ENCODING  
 PAK5 POLYPEPTIDES AND  
 METHODS OF USE THEREOF  
 Inventor(s): Gregory PLOWMAN et al.  
 DOCKET NO.: 034536-1034

**Fig. 9 I**  
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SEQ ID NO: 11 ZC3 HUMAN

GCATTTGGGGAGGTGTATGAGGGTCTGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAG  
GTCATGGATGTCACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAA  
AAGTACTCTCACCACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCC  
CCGGGAAACGATGACCAGCTCTGGCTGGTGTATGGAGTTCTGTGGTGCTGGTTTCAGTGACT  
GACCTGGTAAAGAACAACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGC  
AGGGAGATCCTCAGGGGTCTGGCCCATCTCCATGCCCCACAAGGTGATCCATCGAGACATC  
AAGGGGCAGAATGTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTG  
AGTGCTCAGCTGGACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGG  
ATGGCTCCAGAGGTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGT  
GATATTTGGTCTCTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCTCTGTGT  
GACATGCACCCCATGCGAGCCCTCTTCCTCATTCCCTCGGAACCTCCGCCCAGGCTCAAG  
TCCAAGAAGTGGTCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTAC  
CTGAGCCGCCCCACCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACG  
GAGCGGCAGGTCCGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGT  
GAGAAAGAGGAGACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGA  
GAGGAAGGAGAGCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAG  
TTTCTCCGGCTCCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAG  
CTGCAGCAGCAGCAGCAGCAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGG  
CAGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGG  
GAGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAG  
GCTCTGCGGCGGGAGGAGGAGCGGCGGCAGGCGGAGCGCGAGCAGGAATATATTCTGCAC  
AGGCTAGAGGAGGAGCAGCGACAGCTCGAGATCCTTCAGCAACAGCTGCTCCAGGAACAG  
GCCCTGCTGCTGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTC  
CAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAG  
CAGCAGCTTCAGAAACAACAGCAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTAC  
CATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCCCCGAGAGGTAGAAGAG  
AGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCACG  
GGGCCTGAGCCCCCATCCCCAGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCAGACT  
CCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAAGAGCCTGGTGGCACAC  
CGGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATCCCAGTCCCTGCAGGACCAG  
CCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGACCTGCCATCCCCGCA  
CCCCTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACTCT  
GAAGGACCTGGCCCCAGCCCGAATCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCA  
CCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGA  
GGGTCCCGGCCAGCCAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATC  
TATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCC  
CCTGGCCCCGCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGCGACCTGGCTGGGAA

Title: NUCLEIC ACIDS ENCODING  
PAK5 POLYPEPTIDES AND  
METHODS OF USE THEREOF  
Inventor(s): Gregory PLOWMAN et al.  
DOCKET NO.: 034536-1034

**Fig. 9J**  
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CGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAG  
 CGGAACCGCGTGGGAGTCTCCTCCAAACCGGACAGCTCCCCTGTGCTCTCCCCTGGGAAT  
 AAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTG  
 AAAGAGCGGACTCTGGACGAGGCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCG  
 TCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCCGAAGGCCGGCCAGCA  
 GAGGGGAGCAGAGATACCCCTGGGGGCGCGATGGGGATACAGACAGCGTCAGCACCATG  
 GTGGTCCACGACGTGAGGAGATCACCGGGACCCAGCCCCCATAACGGGGGCGGCACCATG  
 GTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTAC  
 ACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAA  
 AGCCCCACCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCT  
 GGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGG  
 GACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAG  
 TACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCACAGT  
 GAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCC  
 CTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGT  
 GGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTG  
 GAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAACTGCGGGTGTATTAC  
 TTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGC  
 TGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGG  
 ATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAA  
 CCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCACCGCCCTCTGCTG  
 GTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGC  
 TTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATC  
 CAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATG  
 CTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAAGGAT  
 GTGGTGTGCTGAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATA  
 ATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGG  
 GTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTG  
 TTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGT  
 AACCGCATCATGAACTGGTGACGGGGCCCTGGGCTGGGGCTGTCCACACTGGACCCAGC  
 TCTCCCCCTGCAGCCAGGCTTCCCGGGCCGCCCTCTTTCCCTCCCTGGGCTTTTGCTT  
 TTAAGTGGTTTGATTTCACTGGAGCCTGCTGGGAACGTGACCTCTGACCCCTGA

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CAATGTAAACCCACTCTATGTCTCTCCTGCATGTAAAAAACCACTAATCCACATGTATGA  
 AAAGGAGTTCACCTTCTGAGATCTGCTGTGGTTCTTTGTGGGGAGTCAATTTGCTGTTGGG  
 AACCCGATCTAATCTATATCTGATGGACAGAAGTGGAAAGGCTGACATTACTAACTTAT  
 AAGGCCGAAGACCATTCCGCCAGATTCAAGTCTTAGAGCCACTCAATTTGCTGATTACCAT

CTCAGGTCATAAGAACAGACTTCGGGTGTATCATCTGACCTGGTTGAGGAACAAGATTTT  
 GAATAATGATCCAGAAAGTAAAAGAAGGCAAGAAGAAATGCTGAAGACAGAGGAAGCCTG  
 CAAAGCTATTGATAAGTTAACAGGCTGTGAACACTTCAGTGTCTCCAACATGAAGAAAC  
 AACATATATTGCAATTGCTTTGAAATCATCAATTCACCTTTATGCATGGGCACCAAAGTC  
 CTTTGATGAAAGCACTGCTATTAAAGTATTTCCAACACTTGATCATAAGCCAGTGACAGT  
 TGACCTGGCTATTGGTTCTGAAAAAAGACTAAAGATTTTCTTCAGCTCAGCAGATGGATA  
 TCACCTCATCGATGCAGAATCTGAGGTTATGTCTGATGTGACCCTGCCAAAGAATCCCCT  
 GGAAATCATTATACCACAGAATATCATCATTTTACCTGATTGCTTGGGAATTGGCATGAT  
 GCTCACCTTCAATGCTGAAGCCCTCTCTGTGGAAGCAAATGAACAACCTCTTCAAGAAGAT  
 CCTTGAAATGTGGAAAGACATACCATCTTCTATAGCTTTTGAATGTACACAGCGAACCAC  
 AGGATGGGGCCAAAAGGCCATTGAAGTGCGCTCTTTGCAATCCAGGGTTCTGGAAAGTGA  
 GCTGAAGCGCAGGTCAATTAAGAAGCTGAGATTCTGTGCACCCGGGGTGACAAGCTGTT  
 CTTTACCTCTACCCTGCGCAATCACCACAGCCGGGTTTACTTCATGACACTTGGAAAAC  
 TGAAGAGCTCCAAAGCAATTATGATGTCTAAAAGTTTCCAGTGATTTATTACCACATTAT  
 AAACATCATGTATAGGCAGTCTGCATCTTCAGATTTTCAGAGATTAAATGAGTATTCAGTT  
 TTATTTTTAGTAAAGATTAAATCCAAAACCTTTACTTTTAATGTAGCACAGAATAGTTTTA  
 ATGAGAAATGCAGCTTTATGTATAAAATTAAGTATAGCAAGCTCTAGGTACTCCAATGGT  
 GTACAATGTCTTTTGCACAACTTTGTAACCTTTTGTACTGTGAATTCAAACATTACTCT  
 TTGGACAGTTTGGACAGTATCTGTATTTCAGATTTTACAACATGGAGTAAAGAAACCTGTT  
 ATGAATTAGATTACAAGCAGCCTTCAAAGAATTGGCACTGGGATAAGATTTTTCAGAAA  
 AGAAAAACATCGGCCAACT

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CCGCCATGAACCCCGGCTTCGATTTGTCCCGCCGGAACCCGCAGGAGGACTTCGAGCTGA  
 TTCAGCGCATCGGCAGCGGCACCTACGGCGACGTCTACAAGGCACGGAATGTTAACACTG  
 GTGAATTAGCAGCAATTAAAGTAATAAAATTGGAACCAGGAGAAGACTTTGCAGTTGTGC  
 AGCAAGAAATTATTATGATGAAAGACTGTAAACACCCCAAATATTGTTGCTTATTTTGGAA  
 GCTATCTCAGGCGAGATAAGCTTTGGATTTGCATGGAGTTTTGTGGAGGTGGTTCTTTAC  
 AGGATATTTATCACGTAAGTGGACCTCTGTCAGAACTGCAAATTGCATATGTTAGCAGAG  
 AAACACTGCAGGGATTATATTATCTTCACAGTAAAGGAAAAATGCACAGAGATATAAAGG  
 GAGCTAACATTCTATTAACGGATAATGGTCATGTGAAATTGGCTGATTTTGGAGTATCTG  
 CACAGATAACAGCTACAATTGCCAAACGGAAGTCTTTCATTGGCACACCATATTGGATGG  
 CTCCAGAAGTTGCAGCTGTTGAGAGGAAGGGGGTTACAATCAACTCTGTGATCTCTGGG  
 CAGTGGGAATCACTGCCATAGAACTTGCAGAGCTTCAGCCTCCTATGTTTGACTTACACC  
 CAATGAGAGCATTATTTCTAATGACAAAAAGCAATTTTCAGCCTCCTAAACTAAAGGATA  
 AAATGAAATGGTCAAATAGTTTTCATCACTTTGTGAAAATGGCACTTACCAAAAATCCGA  
 AAAAAAGACCTACTGCTGAAAAATTATTACAGCATCCTTTTGTAAACACAACATTTGACAC  
 GGTCTTTGGCAATCGAGCTGTTGGATAAAGTAAATAATCCAGATCATTCCACTTACCATG

**Fig. 9L**  
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ATTTTCGATGATGATGATCCTGAGCCTCTTGTTGCTGTACCATAGAAATTCACCTCAACAA  
 GTAGAAACGTGAGAGAAGAAAAACACGCTCAGAGATAACCTTTGGCCAAGTGAAATTTG  
 ATCCACCCTTAAGAAAGGAGACAGAACCACATCATGAACTTCCCGACAGTGATGGTTTTT  
 TGGACAGTTTCAAGAAATATACTACACTGCAAGATCTAATCTGGATCTGCAACTGGAAT  
 ATGGACAAGGACACCAAGGTGGTTACTTTTTAGGTGCAACAAGAGTCTTCTCAAGTCTG  
 TTGAAGAAGAATTGCATCAGCGAGGACACGTGCGACATTTAGAAGATGATGAAGGAGATG  
 ATGATGAATCTAAACACTCAACTCTGAAAGCAAAAATTCCACCTCCTTTGCCACCAAGC  
 CTAAGTCTATCTTCATACCACAGGAAATGCATTCTACTGAGGATGAAAATCAAGGAACAA  
 TCAAGAGATGTCCCATGTCAGGGAGCCCAGCAAAGCCATCCCAAGTTCCACCTAGACCAC  
 CACCTCCCAGATTACCCCCACACAAACCTGTTGCCTTAGGAAATGGAATGAGCTCCTTCC  
 AGTTAAATGGTGAACGAGATGGCTCATTATGTCAACAACAGAATGAACATAGAGGCACAA  
 ACCTTTCAAGAAAAGAAAAGAAAGATGTACCAAAGCCTATTAGTAATGGTCTTCTCCAA  
 CACCTAAAGTGCATATGGGTGCATGTTTTTCAAAGTTTTTAATGGGTGTCCCTTGAAAA  
 TTCCTGTGCATCATCATGGATAAACCCAGATACAAGAGATCAGTACTTGATATTTGGTG  
 CCGAAGAAGGGATTTATACCCTCAATCTTAATGAACTTCATGAAACATCAATGGAACAGC  
 TATTCCTCGAAGGTGTACATGGTTGTATGTAATGAACAATTGCTTGCTATCAATATCTG  
 GTAAAGCTTCTCAGCTTTATTCCCATAATTTACCAGGGCTTTTTTGATTATGCAAGACAAA  
 TGCAAAAGTTACCTGTTGCTATTCAGCACACAAACTCCCTGACAGAATACTGCCAAGGA  
 AATTTTCTGTATCAGCAAAAATCCCTGAAACCAAATGGTGCCAGAAGTGTTGTGTTGTAA  
 GAAATCCTTACACGGGCCATAAATACCTATGTGGAGCACTTCAGACTAGCATTGTTCTAT  
 TAGAATGGGTTGAACCAATGCAGAAATTTATGTTAATTAAGCACATAGATTTTCTTATAC  
 CATGTCCACTTAGAATGTTTGAAATGCTGGTAGTTCCTGAACAGGAGTACCCTTTAGTTT  
 GTGTTGGTGTGAGTAGAGGTAGAGACTTCAACCAAGTGGTTGATTTGAGACGGTCAATC  
 CAAATTCTACCTCTTCATGGTTTACAGAATCAGATACCCACAGACAAATGTTACTCATG  
 TAACCCAACTGGAGAGAGATAACCATCCTTGTATGCTTGGACTGTTGTATAAAAATAGTAA  
 ATCTCCAAGGAAGATTAAAATCTAGCAGGAAATTGTCATCAGAACTCACCTTTGATTTC  
 AGATTGAATCAATAGTGTGCCTACAAGACAGTGTGCTAGCTTTCTGGAAACATGGAATGC  
 AAGGTAGAAGTTTTAGATCTAATGAGGTAACACAAGAAATTTAGATAGCACAGAATTT  
 TCAGGCTGCTTGGATCTGACAGGGTCGTGGTTTTGGAAAGTAGGCCAACTGATAACCCCA  
 CAGCAAATAGCAATTTGTACATCCTGGCGGGTCATGAAAACAGTTACTGAGAATTGTTGT  
 GCTTTGACAGTTAACTCTAGAAAGAAAGAACTACCACTGCAACATTAATGGATGCTTG  
 AAGCTGTACAAAAGCTGCAGTAACCTGTCTTCAGTTACTTTGTAATTTATTGTGGCATGA  
 GATAAGATGGGGAAAATTTTGTTTTAAAGTGGTATGGATATATTTAGCATATTGAACCACA  
 CAAGTGCTTAATTCATTGTTATGTAATCTTTGTACATATAGGCAGTATTTTTCTGTGAA  
 ACTTCATATTGCTGAAGACATACACTAAGAATTTATGTAGATAATGTACTTTTATGAGAT  
 GTACAAGTAAGTGTCTTATCTGTACAGATGTAAATGTTGATGAAAATGCAATTGGGGTTA  
 ATATTTTAAGAATCTTTAGTATATTCTTGGGTGTGGCTATATTACAAAATGGGATGCTG  
 GCAATGAAACAATACATTTAACAATATTGTATTTTTATTATATGTAATTTAGTAATATGA

ATATAAATCTTGTAACCTTTTAAAATTGTAATGGAGGCTGTAATCATTTTATAATCTTTTT  
AATTTTAATGCAAGTACACTGGTGTATTTATATTTGCACAAAGTATTGATATGTGATGTATT  
AAGTCACAAAAGTAAGCTGTGACATTGTCTATAAGCATTGGCTCCACAAATGTATTTGG  
ATTGTTTTCTATGTGAAGCAAACCAATTATAATTAACCACATGTTGTAGTAACTGGTCTT  
TTTATATTTAAGCAGAATCCTGTAAGATTGCTTGTCTTTGCTTAAAAACAATACCTTTGA  
ACATTTTTGAATCACAGAATAGCGGTACCATGATAGAATACTGCAATTGTGGTCAGAATT  
ACAGTATGCACAAAGAATTAATTAGCATTATTAAGAGAGTCTCACTAAACATTTTCATATG  
ATCACACTGAAGAACTGTAACATTCCATAGAGTGAAGTGGTTCAAATTTCTCTTGGAATT  
TTTACTTTTGTGGCCTTATTTTATGATCCTTTTCATATTTCTTTTGACTTAGAGTATTA  
ATACATGGCCAAAATAATTTAGTTACTACCTCATACAAACAATAATGGTTACTACACA  
TCACAGGAAGCTTAGTTTTGGTTTAAGTCAFTTTTGATTGCTTTTTTCCAATGGAATATGT  
ATATACCAGGTTTTAGCAAAATGCACACTTTTGGCTCTTTTTGGTATATGTTCTTTATAT  
TTTAATGTGAGTATATACACTAAGAACAACCTAAATTGTGATTTATGATCTTCATTTATT  
TTAATGATAATGGTTTTAAATATGTTCTGATTGTACATATTGTAAATAAACATGTTT  
TTT

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GGGAGGGTCCTTGTGGCGCCGGGCGGGGTCCTGCGTGGAGAGTGGGACGCAACGCCG  
AGACCGCGAGCAGAGGCTGCGCACAGCCGGATCCGGCACTCAGCGACCGGACCCAAGGAT  
CCGCCGGGGAACAAGCCACAGGAGAGCGACTCAGGAACAAGTGTGGGAGAGGAAGCGGCG  
GCGGCGGCGCCGGGCCCCGGGGGTGGTGACAGCAGGTCTGAGGTTGCATCATAAATACAAA  
GGACTGAAGTTATAAAAGAGAAAAAGAGAAGTTTGCTGCTAAAATGAATCTGAGCAATATG  
GAATATTTTGTGCCACACACAAAAAGGTACTGAAGATTTACCCCCCAAAAAAATTGTCA  
ATGAGAAATAAAGCTAACTGATATCAAAAAGCAGAGCCTGCTCTACTGGCCATCATGCGT  
AAAGGGGTGCTGAAGGACCCAGAGATTGACGATCTATTCTACAAAGATGATCCTGAGGAA  
CTTTTTATTGGTTTGCATGAAATTGGACATGGAAGTTTTGGAGCAGTTTATTTTGCTACA  
AATGCTCACACCAATGAGGTGGTGGCAATTAAGAAGATGTCCTATAGTGGGAAGCAGACC  
CATGAGAAATGGCAAGATATTCTTAAGGAAGTTAAATTTTTACGACAATTGAAGCATCCT  
AATACTATTGAGTACAAAGGCTGTTACTTGAAAGAACACACTGCTTGGTTGGTGATGGAA  
TATTGCTTAGGCTCAGCCTCTGATTTATTAGAAGTTCATAAAAAACCACTTCAGGAAGTG  
GAGATCGCTGCCATTACTCATGGAGCCTTGCATGGACTAGCCTACCTACATTCTCATGCA  
TTGATTCATAGGGATATTAAAGCAGGAAATATTCTTCTAACAGAGCCAGGTCAGGTAAAA  
CTAGCTGATTTTGGATCTGCTTCAATGGCTTCTCCTGCCAACTCCTTCGTGGGCACACCT  
TACTGGATGGCTCCAGAGGTGATCTTAGCTATGGATGAAGGACAGTATGATGGGAAAGTT  
GATATTTGGTCACTTGGCATCACTTGTATTGAATTGGCGGAACGGAAGCCGCCCTTTTC  
AACATGAATGCAATGAGTGCCTTATATCACATTGCCCAGAATGACTCCCCAACGTTACAG  
TCTAATGAATGGACAGACTCCTTTAGGAGATTTGTTGATTACTGCTTGCAGAAAAATACCT  
CAGGAAAGGCCAACATCAGCAGAACTATTAAGGCATGACTTTGTTTCGACGAGACCGGCCA

CTACGTGTCCTCATTGACCTCATACAGAGGACAAAAGATGCAGTTCGTGAGCTAGATAAC  
 CTACAGTACCGAAAAATGAAAAAATACTTTTCCAAGAGACACGGAATGGACCCTTGAAT  
 GAGTCACAGGAGGATGAGGAAGACAGTGAACATGGAACCAGCCTGAACAGGGAAATGGAC  
 AGCCTGGGCAGCAACCATTCCATTCCAAGCATGTCCGTGAGCACAGGCAGCCAGAGCAGC  
 AGTGTGAACAGCATGCAGGAAGTCATGGACGAGAGCAGTTCCGAACCTTGTCATGATGCAC  
 GATGACGAAAGCACAAATCAATTCCAGCTCCTCCGTGCGTGCATAAGAAAGATCATGTATTC  
 ACAAGGGATGAGGCGGGCCACGGCGATCCCAGGCCTGAGCCGCGGCCTACCCAGTCAGTT  
 CAGAGCCAGGCCCTCCACTACCGGAACAGAGAGCGCTTTGCCACGATCAAATCAGCATCT  
 TTGGTTACACGACAGATCCATGAGCATGAGCAGGAGAACGAGTTGCGGGAACAGATGTCA  
 GGTTATAAGCGGATGCGGCGCCAGCACCAGAAGCAGCTGATCGCCCTGGAGAACAAAGCTG  
 AAGGCTGAGATGGACGAGCACCGCCTCAAGCTACAGAAGGAGGTGGAGACGCATGCCAAC  
 AACTCGTCCATCGAGCTGGAGAAGCTGGCCAAGAAGCAAGTGGCTATCATAGAAAAGGAG  
 GCAAAGGTAGCTGCAGCAGATGAGAAGAAGTTCCAGCAACAGATCTTGGCCCAGCAGAAG  
 AAAGATTTGACAACTTTCTTAGAAAGTCAGAAGAAGCAGTATAAGATTTGTAAGGAAAAA  
 ATAAAAGAGGAAATGAATGAGGACCATAGCACACCCAAGAAAGAGAAGCAAGAGCGGATC  
 TCCAAACATAAAGAGAACTTGCAGCACACACAGGCTGAAGAGGAAAGCCCACCTTCTCACT  
 CAACAGAGACTGTACTACGACAAAAATTGTCGTTTCTTCAAGCGGAAAATAATGATCAAG  
 CGGCACGAGGTGGAGCAGCAGAACATTCGGGAGGAACTAAATAAAAAGAGGACCCAGAAG  
 GAGATGGAGCATGCCATGCTAATCCGGCACGACGAGTCCACCCGAGAGCTAGAGTACAGG  
 CAGCTGCACACGTTACAGAAGCTACGCATGGATCTGATCCGTTTACAGCACCCAGACGGAA  
 CTGGAAAACCAGCTGGAGTACAATAAGAGGGCGAGAAAGAGAACTGCACAGAAAGCATGTC  
 ATGGGACTTCGGCAACAGCCAAAAAACTTAAAGGCCATGGAAATGCAAATTAAAAAACAG  
 TTTCAAGGACACTTGCAAAGTACAGACCAAACAGTATAAAGCACTCAAGAATCACCAGTTG  
 GAAGTTACTCCAAAGAATGAGCACAAAACAATCTTAAAGACACTGAAAGATGAGCAGACA  
 AGAAAACCTTGCCATTTTGGCAGAGCAGTATGAACAGAGTATAAATGAAATGATGGCCTCT  
 CAAGCGTTACGGCTAGATGAGGCTCAAGAAGCAGAATGCCAGGCCTTGAGGCTACAGCTC  
 CAGCAGGAAATGGAGCTGCTCAACGCCTACCAGAGCAAAATCAAGATGCAAACAGAGGCA  
 CAACATGAACGTGAGCTCAGAAAGCTAGAGCAGAGAGTGTCTCTGCGCAGAGCACACCTT  
 GAGCAGAAGATTGAAGAGGAGCTGGCTGCCCTTCAGAAGGAACGCAGCGAGAGAATAAAG  
 AACCTATTGGAAAGGCAAGAGCGAGAGATTGAAACTTTTGACATGGAGAGCCTCAGAATG  
 GGATTTGGGAATTTGGTTACATTAGATTTTCTAAGGAGGACTACAGATGAGATTAAATT  
 TTTTGCCATTTACAAAAAAG  
 AACCACATTCCCCATTTTAACGGGCGTTGCTCTCACTCTCTCTCTCTCTCTCTCTCTCTCT  
 ACATCGTGTCGGACTAGTGCTGTTTATTCTTACTCCATCAGGGGGCCCCCTTCTCCCCC  
 CGTGTCAACTTTTCAAGTGCTGGCCAAAACCTGGCCGTCTCTTCTATTACAGTACACGTCA  
 CAGTATTGATGTGATTCAAAATGTTTCAGTGAAAACCTTTGGAGACAGTTTAAACAAAACC  
 AATAAACCAACAACAAAAAAGTGGATGTATATTGCTTTAAGCAATCACTCATTACCACC  
 AATCTGTGAAAGTAAAGCAAAAAATAATAATAATAAATGCCAAGGGGGAGAGAGACACAA

**Fig. 9 O**  
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SEO ID NO: 20 SULU3 HUMAN

Title: NUCLEIC ACIDS ENCODING  
PAK5 POLYPEPTIDES AND  
METHODS OF USE THEREOF  
Inventor(s): Gregory PLOWMAN et al.  
DOCKET NO.: 034536-1034

**Fig. 9P**  
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GAAGTCTAAAGAACTCCAAATAAAAAAGCAGTTTCAGGATACCTGCAAAATCCAAACCAG  
 ACAGTACAAAGCATTAAGAAATCACCTGCTGGAGACTACACCAAAGAGTGAGCACAAAGC  
 TGTCTGAAACGGCTCAAGGAGGAACAGACCCGGAAATTAGCTATCTTGGCTGAGCAGTA  
 TGATCACAGCATTAAATGAAATGCTCTCCACACAAGCCCTGCGTTTGGATGAAGCACAGGA  
 AGCAGAGTGCCAGGTTTTGAAGATGCAGCTGCAGCAGGAACTGGAGCTGTTGAATGCGTA  
 TCAGAGCAAAATCAAGATGCAAGCTGAGGCACAACATGATCGAGAGCTTCGCGAGCTTGA  
 ACAGAGGGTCTCCCTCCGGAGGGGCACTCTTAGAACAAAAGATTGAAGAAGAGATGTTGGC  
 TTTGCAGAATGAGCGCACAGAACGAATACGAAGCCTGTTGGAACGTCAAGCCAGAGAGAT  
 TGAAGCTTTTGA CTCTGAAAGCATGAGACTAGGTTTTAGTAATATGGTCCTTTCTAATCT  
 CTCCCCTGAGGCATTTCAGCCACAGCTACCCGGGAGCTTCTGGTTGGTCACACAACCTAC  
 TGGGGGTCCAGGACCTCACTGGGGTCATCCCATGGGTGGCCCAACCAAGCTTGGGGCCA  
 TCCAATGCAAGGTGGACCCCAAGCCATGGGGTCACCCTTCAGGGCCAATGCAAGGGGTACC  
 TCGAGGTAGCAGTATGGGAGTCCGCAATAGCCCCCAGGCTCTGAGGGCGGACAGCTTCTGG  
 GGGACGGACGGAGCAGGGCATGAGCAGAAGCACGAGTGTCACTTCACAAATATCCAATGG  
 GTCACACATGTCTTATACATAACTTAATAATTGAGAGTGGCAATTCGCTGGAGCTGTCT  
 GCCAAAAGAACTGCCTACAGACATCATCACAGCAGCCTCCTCACTTGGGTACTACAGTG  
 TGGAAAGCTGAGTGCATATGGTATATTTTATTCATTTTTGTAAAGCGTTCTGTTTTGTGTT  
 TACTAATTGGGATGTCATAGTACTTGGCTGCCGGGTTTGTGTTGTTTGGGGAAATTTTG  
 AAAAGTGGAGTTGATATTAATAATAATGTGTATGTGTGTACATATATACACACACAT  
 ACACATATATTATGCATGTGGTGAAGAATTGGCTAGATAGGGGATTTTTCTGAACACT  
 GCAAAAATAGAACGTAGCAAAATGGCTTCAGTTATCACTTTTGGGTGTCTGTATCCTAAG  
 AAGTTTCTGAAAAGATCTAAAGCCTTTTTATCCCATATCCCAAATTCTTATGAGCCACTC  
 ACAGCAGGCAGCATATGTTGAAATAAGTTATTACTGGTACACACCTGCATTGCCTACCA  
 GTGTATTTATTTGTTATTAAATTGATCTGACTTCTCAGCCTCATTGGAATAAAAAAGA  
 AAGCAGAAATCCATGAACACATTGCTTCTCGGCCTTTTGGCTAAGATCAAGTGTAGAAAT  
 CCATGAACACTAAAGGACTTCATTGATTTTTTCAGAGAGTAGAAAACAACCTTAGTTTTTC  
 TTTTTCTGAAATGCGTCATAGGCTTGTGAGTGATTTTTGTCCATTCAATTGTGCCTTCT  
 TTGTATTATGATAAGATGGGGGTACTTAAGGAGATCACAAGTTGTGTGAGGATTGCATTA  
 ACAAACCTATGAGCCTTCAATGGGGAAGACCAGAAGGGTGAGAGGGGGCCCTGAAAGTTCA  
 TATGGTGGGTATGTCCCGCAGCAGAGTGAGGAGATGAAGCTTACGTGTCCTGACGTTTTG  
 TTGCTTATACTGTGATATCTCATCCTAGCTAAGCTCTATAATGCCCAAGACCCCAAACAG  
 TACTTTTACTTTGTTTGTACAAAAACAAAGACATATAGCCAATACAAATCAAATGCCGGA  
 GGTGTTTGATGCCATATTTGCAAATTGCCATCTATTGAAATTCTCGTCACACTACATAGA  
 CATAATTGTTATCTCCTTTTGGCTTATGTGATTTTTCTGTTTACAAGTAGAATAGCCAATT  
 ATTTAAATGTTTAGTTGCCACAGTGAACCAGGAGTCACTGAGCCAATGACTTTACCAGCT  
 GCTGACTAATCTTCATCACCCTGTAGATTTTTGCTGCATGTGCAGGTCCTCTATTTTTAA  
 TTGCTGTTTTCGTTGCTGCAGTACTTTACAACTTCTAGTTGTTGAGACTTAGTGACCA  
 TTTGGCATCAAGTTAACATCACACAATAGGAAACACCACTTCCACAAGTCTCAAGCCTCA

Title: NUCLEIC ACIDS ENCODING  
 PAK5 POLYPEPTIDES AND  
 METHODS OF USE THEREOF  
 Inventor(s): Gregory PLOWMAN et al.  
 DOCKET NO.: 034536-1034

**Fig. 9Q**  
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GTGCTAAAGTACTACTGAAAAGGAACTAGGAAGTTTGGCCAATT

SEQ ID NO: 21 SULU3 MURINE

GCAGGATGCCATCAACTAACAGAGCAGGCAGTCTAAAGGACCCTGAAATTGCAGAGCTCT  
TCTTCAAAGAAGATCCGGAAAAGCTCTTCACAGATCTCAGAGAAATCGGCCATGGGAGCT  
TTGGAGCAGTATATTTTGCACGAGATGTGCGTACTAATGAAGTGGTGGCCATCAAGAAAA  
TGTCTTATAGTGGAAGCAGTCTACTGAGAAATGGCAGGATATTATTAAGGAAGTCAAGT  
TTCTACAAAGAATAAAACATCCCAACAGTATAGAATACAAAGGCTGCTATTTACGTGAAC  
ACACAGCATGGCTTGTAATGGAATATTGTTTAGGATCTGCTTCAGATTTATTAGAAGTTC  
ATAAAAAGCCATTACAAGAAGTGGAAATAGCAGCAATTACACATGGTGCTCTCCAGGGAC  
TAGCTTATTTACATTCTCATAACCATGATCCATAGAGATATCAAAGCAGGAAATATCCTTC  
TGACAGAACCAGGCCAAGTGAAACTTGCTGACTTTGGATCTGCTTCCATGGCTTCCCCTG  
CCAATTCTTTTGTGGGAACACCATATTGGATGGCCCCAGAAGTAATTTTAGCCATGGATG  
AAGGACAGTATGATGGCAAAGTTGATGTATGGTCTCTTGGAATAACGTGTATTGAATTAG  
CCGAGAGGAAGCCTCCTTTATTTAATATGAATGCAATGAGTGCCTTATATCACATAGCCC  
AAAATGAATCCCCTACACTACAATCTAATATGAATGATTCTTGCCTCCAGAAAATCCCTC  
AAGATCGCCCTACATCAGAGGAACTTTTAAAGCACATGTTTGTTCCTTCGAGAGCGCCCTG  
AAACAGTGTTAATAGATCTTATTCAAAGGACAAAGGATGCAGTAAGAGAGCTGGACAATC  
TGCAGTATCGAAAGATGAAGAACTCCTTTTCCAGGAGGCACATAATGGGCCAGCGGTAG  
AAGCACAGGAAGAAGAGGAGGAGCAAGATCATGGTGTGGCCGAACAGGAACAGTGAATA  
GTGTTGGAAGCAATCAGTCTATCCCTAGTATGTCTATCAGTGCCAGCAGTCAAAGCAGCA  
GTGTTAATAGTCTTCCAGATGCATCAGATGACAAGAGTGAGCTAGACATGATGGAGGGAG  
ACCATACAGTGATGTCTAACAGTTCTGTCTATCCACTTAAACCTGAGGAGGAAAATTACC  
AGGAAGAAGGAGATCCTAGAACAAAGAGCATCAGACCCACAGTCTCCCCCTCAGGTGTCTC  
GTCACAAGTCACATTATCGTAATAGAGAACACTTTGCAACCATACGAACAGCATCACTGG  
TTACAAGACAGATGCAAGAACATGAGCAGGACTCTGAACTTAGAGAACAGATGTCTGGTT  
ATAAGCGGATGAGGCGACAGCATCAAAAGCAGCTGATGACGCTGGAAAATAAACTGAAGG  
CAGAGATGGACGAACATCGGCTCAGATTAGACAAAGATCTTGAAACTCAGCGTAACAATT  
TCGCTGCAGAAATGGAGAACTTATTAAGAAACACCAAGCTGCTATGGAAAAAGAGGCTA  
AAGTGATGGCCAATGAGGAGAAAAAATTCCAGCAACACATTCAGGCTCAACAGAAAAAAG  
AACTGAATAGCTTTTTTGGAGTCTCAAAAAAGAGAATATAAACTTCGCAAAGAGCAGCTTA  
AGGAGGAGCTGAATGAAAACCAGAGCACACCTAAAAAAGAAAAGCAGGAATGGCTTTCAA  
AGCAGAAGGAGAATATACAGCATTTTCAGGCAGAAGAAGAAGCTAATCTTCTTCGACGTC  
AAAGGCAGTATCTAGAGCTAGAATGTCGTCGCTTCAAAAGAAGAATGTTACTTGGGCGAC  
ATAACTTGGAACAGGACCTTGTCAGGGAGGAGTTAAACAAAAGGCAGACTCAAAGGACT  
TGGAACATGCAATGCTATTGCGACAGCATGAATCAATGCAAGAACTGGAGTTTCGCCATC  
TCAACACTATTGAGAAGATGCGCTGTGAGTTGATCAGACTGCAGCATCAAAGTGAAGCTCA  
CTAACCAGCTAGAGTACAATAAGAGAAGGGAACGGGAAGTGAAGGCGAAAACATGTCATGG

AAGTTCGACAACAACCTAAGAGTCTGAAGTCTAAAGAACTCCAAATAAAAAAGCAGTTTC  
AGGATACCTGCAAAATTCAAAACAGACAGTACAAAGCATTAAAGGAATCACCTACTGGAGA  
CTACACCAAAGAATGAGCACAAAGCAATC

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CGAAGCCACAGCCCGAGCCCGAGCCCGAGCCCGAGCCGGCGCCACCGCGCCCCCGGCCAT  
GGCTTTTGGCAATTTCCGCCGCATCCTGCGCCTGTCTACCTTCGAGAAGAGAAAGTCCCG  
CGAATATGAGCACGTCCGCCGCGACCTGGACCCCAACGAGGTGTGGGAGATCGTGGGCGA  
GCTGGGCGACGGCGCCTTCGGCAAGGTTTACAAGGCCAAGAATAAGGAGACGGGTGCTTT  
GGCTGCGGCCAAAGTCATTGAAACCAAGAGTGAGGAGGAGCTGGAGGACTACATCGTGGA  
GATTGAGATCCTGGCCACCTGCGACCAACCCCTACATTGTGAAGCTCCTGGGAGCCTACTA  
TCACGACGGGAAGCTGTGGATCATGATTGAGTTCTGTCCAGGGGGAGCCGTGGACGCCAT  
CATGCTGGAGCTGGACAGAGGCCTCACGGAGCCCCAGATACAGGTGGTTTGGCGCCAGAT  
GCTAGAAGCCCTCAACTTCCTGCACAGCAAGAGGATCATCCACCGAGATCTGAAAGCTGG  
CAACGTGCTGATGACCCTCGAGGGAGACATCAGGCTGGCTGACTTTGGTGTGTCTGCCAA  
GAATCTGAAGACTCTACAGAAACGAGATTCTTTCATCGGCACGCCTTACTGGATGGCCCC  
CGAGGTGGTCATGTGTGAGACCATGAAAGACACGCCCTACGACTACAAAGCCGACATCTG  
GTCCCTGGGCATCACGCTGATTGAGATGGCCCAGATCGAGCCGCCACACCACGAGCTCAA  
CCCCATGCGGGTCCTGCTAAAGATCGCCAAGTCGGACCCTCCCACGCTGCTCACGCCCTC  
CAAGTGGTCTGTAGAGTTCCGTGACTTCCTGAAGATAGCCCTGGATAAGAACCCAGAAAC  
CCGACCCAGTGCCGCGCAGCTGCTGGAGCATCCCTTCGTCAGCAGCATCACCAGTAACAA  
GGCTCTGCGGGAGCTGGTGGCTGAGGCCAAGGCCGAGGTGATGGAAGAGATCGAAGACGG  
CCGGGATGAGGGGGAAGAGGAGGACGCCGTGGATGCCGCCTCCACCCTGGAGAACCATAC  
TCAGAACTCCTCTGAGGTGAGTCCGCCAAGCCTCAATGCTGACAAGCCTCTCGAGGAGTC  
ACCTTCCACCCCGCTGGCACCCAGCCAGTCTCAGGACAGTGTGAATGAGCCCTGCAGCCA  
GCCCTCTGGGGACAGATCCCTCCAAACCACCAAGTCCCCCAGTCGTGGCCCCCTGGAAATGA  
GAACGGCCTGGCAGTGCCCTGTGCCCCTGCGGAAGTCCCGACCCGTGTCAATGGATGCCAG  
AATTCAGGTAGCCCAGGAGAAGCAAGTTGCTGAGCAGGGTGGGGACCTCAGCCCAGCAGC  
CAACAGATCTCAAAAGGCCAGCCAGAGCCGGCCCAACAGCAGCGCCCTGGAGACCTTGGG  
TGGGGAGAAGCTGGCCAATGGCAGCCTGGAGCCACCTGCCCAGGCAGCTCCAGGGCCTTC  
CAAGAGGGACTCGGACTGCAGCAGCCTCTGCACCTCTGAGAGCATGGACTATGGTACCAA  
TCTCTCCACTGACCTGTCGCTGAACAAAGAGATGGGCTCTCTGTCCATCAAGGACCCGAA  
ACTGTACAAAAAACCTCAAGCGGACACGCAAATTTGTGGTGGATGGTGTGGAGGTGAG  
CATCACCACTCCAAGATCATCAGCGAAGATGAGAAGAAGGATGAGGAGATGAGATTTCT  
CAGGCGCCAGGAACTCCGAGAGCTTCGGCTGCTCCAGAAAGAAGAGCATCGGAACCAGAC  
CCAGCTGAGTAACAAGCATGAGCTGCAGCTGGAGCAAATGCATAAACGTTTTGAACAGGA  
AATCAACGCCAAGAAGAAGTTCTTTGACACGGAATTAGAGAACCTGGAGCGTCAGCAAAA  
GCAGCAAGTGGAGAAGATGGAGCAAGACCATGCCGTGCGCCGCCGGGAGGAGGCCAGGCG

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**Fig. 9S**  
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GATCCGCCTGGAGCAGGATCGGGACTACACCAGGTTCCAAGAGCAGCTCAAACCTGATGAA  
GAAAGAGGTGAAGAACGAGGTGGAGAAGCTCCCCCGACAGCAGCGGAAGGAAAGCATGAA  
GCAGAAGATGGAGGAGCACACGCAGAAAAAGCAGCTTCTTGACCGGGACTTTGTAGCCAA  
GCAGAAGGAGGACCTGGAGCTGGCCATGAAGAGGCTCACCACCGACAACAGGCGGGGAGAT  
CTGTGACAAGGAGCGCGAGTGCCTCATGAAGAAGCAGGAGCTCCTTCGAGACCGGGGAAGC  
AGCCCTGTGGGAGATGGAAGAGCACCAGCTGCAGGAGAGGCACCAGCTGGTGAAGCAGCA  
GCTCAAAGACCACTACTTCCTCCAGCGGCACGAGCTGCTGCGCAAGCATGAGAAGGAGCG  
GGAGCAGATGCAGCGCTACAACCAGCGCATGATAGAGCAGCTGAAGGTGCGGCAGCAACA  
GGAAAAGGCGCGGCTGCCCAAGATCCAGAGGAGTGAGGGCAAGACGCGCATGGCCATGTA  
CAAGAAGAGCCTCCACATCAACGGCGGGGGCAGCGCAGCTGAGCAGCGTGAGAAGATCAA  
GCAGTTCTCCCAGCAGGAGGAGAAGAGGCAGAAGTCGGAGCGGCTGCAGCAACAGCAGAA  
ACACGAGAACCAGATGCGGGACATGCTGGCGCAGTGCAGAGCAACATGAGCGAGCTGCA  
GCAGCTGCAGAATGAAAAGTGCCACCTCCTGGTAGAGCACGAAACCCAGAAACTGAAGGC  
CCTGGATGAGAGCCATAACCAGAACCTGAAGGAAT

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CGTTCCTGGGCTTCCCGCTCCGCAGGCCTGCGGAGGACTGGCCCAGCAAGGTCCCAGGTC  
TTCCCTCTCCTTAGCGCCTAAGAGAGAGGGCCAGTGCGGGTGAGGAGTCGCGAGGGAAGAG  
GCGGAAGGCGCCGGAAGGCACCATGTTCCGCAAGAAAAAGAAGAAACGCCCTGAGATCTC  
AGCGCCACAGAACTTCCAGCACCGTGTCCACACCTCCTTCGACCCCAAAGAAGGCAAGTT  
TGTGGGCCTCCCCCACAATGGCAGAACATCCTGGACACACTGCGGGCGCCCCAAGCCCGT  
GGTGGACCCTTCGCGAATCACACGGGTGCAGCTCCAGCCCATGAAGACAGTGGTGCGGGG  
CAGCGCGATGCCTGTGGATGGCTACATCTCGGGGCTGCTCAACGACATCCAGAAGTTGTC  
AGTCATCAGCTCCAACACCCTGCGTGGCCGCAGCCCCACCAGCCGGCGGGGCACAGTC  
CCTGGGGCTGCTGGGGGATGAGCACTGGGCCACCGACCCAGACATGTACCTCCAGAGCCC  
CCAGTCTGAGCGCACTGACCCCCACGGCCTTACCTCAGCTGCAACGGGGGACACACCAGC  
AGGCCACAAGCAGATGCCGTGGCCCGAGCCACAGAGCCACGGGTCTGCCCAATGGGCT  
GGCTGCAAAGGCACAGTCCCTGGGCCCCGCGAGTTTCAGGGTGCTTCGCAGCGCTGTCT  
GCAGCTGGGTGCCTGCCTGCAGAGCTCCCCACCAGGAGCCTCGCCCCCACGGGCACCAA  
TAGGCATGGAATGAAGGCTGCCAAGCATGGCTCTGAGGAGGGCCCGGCCACAGTCCTGCCT  
GGTGGGCTCAGCCACAGGCAGGCCAGGTGGGGAAGGCAGCCCTAGCCCTAAGACCCGGGA  
GAGCAGCCTGAAGCGCAGGCTATTCCGAAGCATGTTCTGTCCACTGCTGCCACAGCCCC  
TCCAAGCAGCAGCAAGCCAGGCCCTCCACCACAGAGCAAGCCCCAACTCCTCTTTCCGACC  
GCCGCAGAAAGACAACCCCCCAAGCCTGGTGGCCAAGGCCCAGTCCTTGCCCTCGGACCA  
GCCGGTGGGGACCTTCAGCCCTCTGACCACTTCGGATAACAGCAGCCCCCAGAAGTCCCT  
CCGCACAGCCCCGGCCACAGGCCAGCTTCCAGGCCGGTCTTCCCCAGCGGGATCCCCCG  
CACCTGGCACGCCCAGATCAGCACCAAGCAACCTGTACCTGCCCCAGGACCCCCACGGTTGC  
CAAGGGTGCCCTGGCTGGTGGAGACACAGGTGTTGTGACACATGAGCAGTTCAAGGCTGC

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**Fig. 9T**  
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GCTCAGGATGGTGGTGGACCAAGGGTGACCCCCGGCTGCTGCTGGACAGCTACGTGAAGAT  
 TGGCGAGGGGCTCCACCGGCATCGTCTGCTTGGCCCCGGGAGAAGCACTCGGGCCGCCAGGT  
 GGCCGTCAAGATGATGGACCTCAGGAAGCAGCAGCGCAGGGAGCTGCTCTTCAACGAGGT  
 GGTGATCATGCGGGACTACCAGCACTTCAACGTGGTGGAGATGTACAAGAGCTACCTGGT  
 GGGCGAGGAGCTGTGGGTGCTCATGGAGTTCCTGCAGGGAGGAGCCCTCACAGACATCGT  
 CTCCCAAGTCAGGCTGAATGAGGAGCAGATTGCCACTGTGTGTGAGGCTGTGCTGCAGGC  
 CCTGGCCTACCTGCATGCTCAGGGTGTCTATCCACCGGGACATCAAGAGTGACTCCATCCT  
 GCTGACCCTCGATGGCAGGGTGAAGCTCTCGGACTTCGGATTCTGTGCTCAGATCAGCAA  
 AGACGTCCCTAAGAGGAAGTCCCTGGTGGGAACCCCCCTACTGGATGGCTCCTGAAGTGAT  
 CTCCAGGTCTTTGTATGCCACTGAGGTGGATATCTGGTCTCTGGGCATCATGGTGATTGA  
 GATGGTAGATGGGGAGCCACCGTACTTCAGTGACTCCCCAGTGCAAGCCATGAAGAGGCT  
 CCGGGACAGCCCCCACCACAAGCTGAAAACTCTCACAAGGTCTCCCCAGTGCTGCGAGA  
 CTTCTGGAGCGGATGCTGGTGCAGGACCCCCAAGAGAGAGCCACAGCCCAGGAGCTCCT  
 AGACCACCCCTTCCTGCTGCAGACAGGGCTACCTGAGTGCCTGGTGCCCTGATCCAGCT  
 CTACCGAAAGCAGACCTCCACCTGCTGAGCCCACCCCAAGTATGCCTGCCACCTACGCCC  
 ACAGGCAGGGCACACTGGGCAGCCAGCCTGCCGGCAGGACTTGCTGCTCCTCCTCTCA  
 GTATTCTCTCAAAGATTGAAATGTGAAGCCCCAGCCCCACCCTCTGCCCTTCAGCCTAC  
 TGGGCCAGGCCGGACCTGCCCCCTCAGTGTCTCTCCCTCCCGAGTCCCCAGATGGAGACC  
 CCTTTCTACAGGATGACCCCTTGATATTTGCACAGGGATATTTCTAAGAAACGCAGAGGC  
 CAGCGTTCCTGGCCTCTGCAGCCAACACAGTAGAAAAGGCTGCTGTGGTTTTTTAAAGGC  
 AGTTGTCCACTAGTGTCTTAGGCCACTGCAGAGGGCAGACTGCTGGTCTCCACAGATACC  
 TGCTGTTCTCAGCTCCAGCTTCAAACCTCGAGTCTCGAGAGGGCCACGGGGTGGTTTTTA  
 TGACCGGAATCCCGCTTCCTCCCTCACGTCTGATGTCCTGAAGGTGCAGTCCCACCTGTA  
 CAGCCCCCTCCCCGCCAAGAACTGTGAATGGCCTGCTCCAGGCCATGGCTGGGGGCAGGGA  
 GTGAGGGGACAATTTCTGAGTGAAAGAGAAAGAATGGGGTGGGTGGTGAAGGTGCTCTCA  
 CTTTACAGAATGGAGAGAACATCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG  
 TG  
 TG  
 CCTCCAGGTCACCCACAGCCAGTTTCAGGAAGGCTGCCCCCTCTCTCCCACTAAGTTCTGG  
 CCTGAAGGGACCTGCTTTCTTGGCCTGGCTTCCACCTCTCCACTCCTGTGTCTACCTGGC  
 CAGTGGAGTGGTCCATGCTAAGTCTAACACTCCTGGGAGCTCAGGAGGCTTCTGAGCTTC  
 TCCTGTACTGTGCATCGTGAGGGCCAGAGACAGGAATGTAAGGATTGGCAACTGTGTTAC  
 CTTTCAAGTTTATCTCAATAACCAGGTCATCAGGGACCCATTGTTCTCTTCAGAACCTTA  
 TCTGGGAGAGAAGGCGAACCACCTCCGGGTTTCCATCATGTCAAGGTCACAGGCATCCAT  
 GTGTGCAAACCATCTGCCCCAGCTGCCTCCACAGACTGCTGTCTCCTTGTCTCCTCGGC  
 CCTGCCCCACTTCAGGGCTGCTGTGAGATGGAATTCCAGGAAAGAACTTCAGGTGTCTGG  
 ACCCTTTCTATCTAGATAATAATTTTATAGATTCTTCTGCTCCCTAGTGACCTACCTGGGGG  
 CAAAGAAATTGCAAGGACTTTTTTTTAAAGGGTCAGAGTTTTTCAAAACAAAAGCATCTTCC  
 CTAGAAATTTTTGTGAATTGTTTGCACCTTGTGCCTGTTTTAAATTAAATTGAGTGTTCAA

AGCC

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GGCCAGTGGGGCGAACTGGCAGCTGGCCGGCCCTTTAACACCTACCCGAGGGCTGACAC  
GGACCACCCATCCCGGGGTGCCCAGGGGGAGCCTCATGACGTGGCCCTAACGGGGCCATC  
AGCGGGGGGCTGGCCATCCCCAGTCCTCCTCCTCCTCCTCCCGGCCTCCCACCCGAGC  
CCGAGGTGCCCCCAGCCCTGGAGTGCTGGGACCCCCACGCCTCAGAGCCCCAGCTGGCCCC  
TCCAGCCTGCACCCCCGCCGCCCTGCTGTTCTTGGGCCCCCTGGCCCCCGCTCACCACA  
GCGGGAGCCACAGCGAGTATCCCATGAGCAGTTCCGGGCTGCCCTGCAGCTGGTGGTGGA  
CCCAGGCGACCCCCGCTCCTACCTGGACAACTTCATCAAGATTGGCGAGGGCTCCACGGG  
CATCGTGTGCATCGCCACCGTGCGCAGCTCGGGCAAGCTGGTGGCCGTCAAGAAGATGGA  
CCTGCGCAAGCAGCAGAGGCGCGAGCTGCTCTTCAACGAGGTGGTAATCATGAGGGACTA  
CCAGCACGAGAATGTGGTGGAGATGTACAACAGCTACCTGGTGGGGGACGAGCTCTGGGT  
GGTCATGGAGTTCCTGGAAGGAGGCGCCCTCACCGACATCGTCACCCACACCAGGATGAA  
CGAGGAGCAGATCGCGGCCGTGTGCCTTGCAGTGCTGCAGGCCCTGTGGTGCTCCACGC  
CCAGGGCGTCATCCACCGGGACATCAAGAGCGACTCGATCCTGCTGACCCATGATGGCAG  
GGTGAAGCTGTCAGACTTTGGGTTCTGCGCCCAGGTGAGCAAGGAAGTGCCCCGAAGGAA  
GTCGCTGGTCGGCACGCCCTACTGGATGGCCCCAGAGCTCATCTCCCGCCTTCCCTACGG  
GCCAGAGGTAGACATCTGGTCGCTGGGGATAATGGTGATTGAGATGGTGGACGGAGAGCC  
CCCCTACTTCAACGAGCCACCCCTCAAAGCCATGAAGATGATTCGGGACAACCTGCCACC  
CCGACTGAAGAACCTGCACAAGGTGTCGCCATCCCTGAAGGGCTTCTTGGACCGCCTGCT  
GGTGCGAGACCCTGCCCAGCGGGCCACGGCAGCCGAGCTGCTGAAGCACCCATTCTGGC  
CAAGGCAGGGCCGCCTGCCAGCATCGTGCCCTCATGCGCCAGAACCGCACCCAGATGAGG  
CCCAGCGCCCTTCCCCTCAACCAAAGAGCCCCCCCCGGGTACCCCCGCCCCACTGAGGCC  
AGTAGGGGGCCAGGCCTCCCCTCCTCCAGCCCCGGGAGATGCTCCGCGTGGCACCACCC  
TCCTTGCTGGGGGTAGATGAGACCCTACTACTGAACTCCAGTTTTGATCTCGTGACTTTT  
AGAAAAACACAGGGACTCGTGGGAGCAAGCGAGGCTCCCAGGACCCCCACCCTCTGGGAC  
AGGCCCTCCCCCATGTTCTTCTGTCTCCAGGAAGGGCAGCGGCCCTCCCATCACTGGAAG  
TCTGCAGTGGGGGTGCTGGGGGTGGAGAGAACTAAGAGGTGAACATGTATGAGTGTG  
TGCACGCGTGTGAGTGTGCATGTGTGTGTGTGTGCAAAGGTCCAGCCACCCCGTCTCCA  
GCCCCGAAGGGGTGTCTGGCGCCTTGCTGACACCCAGCCCCCTCTCCCCCTGAGCCATT  
GTGGGGGTGATCATGAATGTCCGAAGAGTGGCCTTTTCCCGTAGCCCTGCGCCCCCTTT  
CTGTGGCTGGATGGGGAGACAGGTCAGGGCCCCCCCCACCCTCTCCAGCCCCCTGCAGCAAT  
GACTACTGCACCTGGACAGCCTCCTCTTTTCTAGAAGTCTATTTATATTGTCATTTTATA  
ACACTCTAGCCCCTGCCCTTATTGGGGGACAGATGGTCCCTGTCTTGCGGGGTGGCCCTG  
GCAGAACCACTGCCTGAAGAACCAGGTTCTTGGCCGGTCAGCGCAGCCCCAGCCCGCCCA  
CCCCTGCCTCGAGTTAGTTTTACAATTAACATTGTCTTGTGTTTTGTGAAAAAAAAAAAA  
AAAAAAAAAA

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**Fig. 9V**  
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>STLK5\_h

MSSFLPEGGCYELLTVIGKGFEDLMTVNLARYKPTGEYVTVRRINLEACSNEMVTFLLQGELHVSKLFNHPNIVPYRATFI  
ADNELWVVTSMAYGSAKDLICTHFMDSGMNELAIAYILQGVLKALDYIHHMGYVHRSVKASHILISVDGKVYLSGLRSNL  
SMISHGQRQRVVHDFPKYSVKVLPWLSPEVLQQNLQGYDAKSDIYSVGITACELANGHVPFKDMPATQMLLEKLNQGVPC  
LLDTSTIPAEELTMSPSRSVANSGLSDSLTTSTPRPSNGDSPSHPHYHRTFSPHFHFVEQCLQRNPDARPSASTLLNHSF  
FKQIKRRASEALPELLRPVTPITNFEGSQSDHSGIFGLVTNLEEELEVDDWEF

>STLK6\_h

MSLLDCFCTSRTOVESLRPEKQSETSIHQYLVDEPTLSWSRPSTRASEVLCSTNVSHYELQVEIGRGFDNLTSVHLARHT  
PTGTLVTIKITNLENCNEERLKAQKAVILSHFFRHPNITTYWTVFTVGSWLWVISPFMAYGSAQQLLRTYFPEGMSETL  
IRNILFGAVRGLNYLHQNGCIHRSIKASHILISGDLVTL SGLSHLSLVKHGQRHRAVDYDFPQFSTSVQPWLSPELLRQ  
51DLHGYNVKS DIYSVGITACELASGQVPFQDMHRTQMLLQKLKPPYSPLDISIFPQSESRMKNSSQSGVDSGIGESVLVSS  
515/76GTHTVNSDRLHTPSSKTFSPAFFSLVQLCLQQDPEKRPSASSLLSHVFFKQMKESQDSILSLLPPAYNKPSISLPPVLP  
WTEPECDFPDEKDSYWEF

>STLK7\_h

NRDDYELQEVIGSGATAVVQAA YCAPKKEKVAIKRINLEKQCQTSMDLELLKEIQAMSQCHHPNIVSYTTSFVVKDELWLVM  
KLLSGGSVLDIIKHIVAKGEHKS

>ZC4\_h

MAGPGGWRDREVDLGHLPDPTGIFSLDKTIGLGTYGRIYGLGHEKTGAVKVMNARKDEEEDLRTLENLRLKYSFHK  
NIVSFYGAFFKLSPPGQRHQLWMVMELCAAGSVTDVVRMTSNQSLKEDWIA YICREILQGLAHLHAHRV IHRDIKGNVNL  
LTHNAEVKLVD FGVSAQVSRINGRRNSFIGTPYWMapeVIDCDEDPRRSYDYRSDVSWVGITAIEMAE GAPPLCNLQPLE  
ALFVILRESAPT VKSSGWSRKFFHFM EKCTIKNFLFRPTSANMLQHPFVRDIKNERHVVESLTRHLTGI IKKRQKKEQAR  
EKSKSVSTLRQALAKRLSPKRFRAKSSWRPEKLELSDLEARRQRQRWEDIFNQHEEELRQVDKDESSDNDEVFHS

Fig. 10A

IQAEVQIEPLKPYISNPKKIEVQERSPSVPNNQDHAHHVKFSSVPPQRSLLLEQAQKPIDIRQRSSQNRQNWLAASGDSKH  
KILAGKTQSYCLTIYISEVKKEEFQEGMNQKCQGAQVGLGPEGHCIWQLGESSSEESPTGRRSQSSPPYSTIDQKLLV  
DIHVPDGFVKISPPVYLTNEWVGYNALSEIFRNDWLTAPAVIQPPEEDGDYVELYDASADTDGDDDDDESNDTFEDTYD  
HANGNDDLDNQVDQANDVCKDHDNNKFVDDVNNNYEAPSCPRASYGRDGSCKQDGYDGSRGKEEAYRGYGSHTANRS  
HGGSAASEDNAIGDQEEHAANIGSERRGSEGGGKGVVRTSEESGALGLNGEENCSETDGPGLKRPASQDFEYLQEEPG  
GGNEASNAIDSGAAPSAPDHESDNKDISESSTQSDFSANHSSPSKSGMSADANFASAILYAGFVEVPEESPQKQSEVNV  
NPLYVSPACKKPLIHMYEKEFTSEICCGSLWGVNLLGTRSNLYLMDRSGKADITKLIRRRPFRQIQVLEPLNLLITISG  
HKNRLRVYHLTWLRNKILNNDPESKRQRQEEMLKTEEACKAIDKLTGCEHFSVLQHEETTYIAIALKSSIHLYAWAPKSF  
ESTAIVFPTLDHKPVTVDLAIGSEKRLKIFFSSADGYHLIDAESEVMSDVTLPKNPLEIIIPQNIILPDCLGIGMMLT  
FNAEALSVEANEQLFKKILEMWKDIPSSIAFECTQRTTGWGQKAEIVRSLSQSRVLESELKRRSIKKLRFCLTRGDKLFFT  
STLRNHHSRVYFMTLGKLEELQSNYDV

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>PAK5\_h

MFGKRKRKREISAPSNFEHRVHTGFDQHEQKFTGLPRQWQSLIEESARRPKPLVDPACITSIQPGAPKTIVRGSKGAKDG  
ALTLLDEFENMSVTRNSLRRDSPPPPARARQENGMPPEEPATTARGGPGKAGSRGRFAGHSEAGGSGDRRRRAGPEKRP  
KSSREGSGGPQESSRDKRPLSGPDVGTQPAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVAPNGPSAGGLAIP  
QSSSSSRPPTRARGAPSPGVLGPHASEPQLAPPACTPAAPAVPGPPRSPQREPQRVSHREQFRAALQLVDPDPRSY  
LDNFIKIGEGSTGIVCIATVRSSGKLVAVKKMDLRKQQRRELLFNEVIMRDYQHENVVEMYNLYLVGDELWVWMEFLEG  
GALTDIVTHTRMNEEQIAAVCLAVLQALSVLHAQGVHRDIKSDSILLTHDGRVKLSDFGCAQVSKEVPRRKSLVGTPY  
WMAPELISRLPYGPEVDIWSLIGIMVEMVDGEPYPFNEPPLKAMKMIRDNLPPRLKNLHKVSPSLKGFLLDRLLVRDPAQR  
ATAAELLKHPFLAKAGPPASIVPLMRQNRT

>GEK2\_h

MAFANFRRIILRLSTFEKRKSREYEHVRRDLDPNEVWEIVGELGDGAFGKVYKAKNKETGALAAAKVIETKSEEELEDYIV  
EIEILATCDHPYIVKLLGAYYHDGKLLWIMIEFCPGGAVDAIMLELDRLGLTEPQIQVVCQRMLEALNFLHSKRIIHRDLKA

Fig. 10B



GNVLMTLEGDIRLADFGVSAKNLKTLLQKRDSFIGTPTYYWMAPEVVMCETMKDTPYDYKADIWSLGITLIEMAQIEPPHHHEL  
NPMRVLLKIAKSDPPTLLTPSKWSVEFRDFLKIALDKNPETRPSAAQLLEHPFVSSITSNKALRELVAEAKAEVMEEIED  
GRDEGEEDAVDAASTLENHTQNSSEVSPPSLNADKPLEESPSTPLAPSQDSQSVNEPCSPSGDRSLQTTSPPVVAPGN  
ENGLAVPVPLRKSRPVSMMDARIQVAQEKQVAEQGGDLSPAANRSQKASQSRPNSSALETLGGEKLANGSLEPPAQAAPGP  
SKRSDCSSLCTSESMDYGTNLSTDLNLKEMGSLSIKDPKLYKKTLLKTRKFVVDGVEVSIITTSKIISEDEKKDEEMRF  
LRRQELRELRLQKEEHRNQTQLSNKHELQLEQMHRFEQEINAKKKFFDTELENLERQQKQVEKMEQDHA VRRREEAR  
RIRLEQDRDYTRFQEQKLMKKEVKNEVEKLPRQQRKESMKQMEEHTQKKQLLDRDFVAKQKEDLEAMKRLTTDNRRRE  
ICDKERECMKKQELLRDREAA LWEMEEHQLQERHQLVKQQLKDQYFLQRHELLRKHEKEREQMQRYNQRMIEQLKVRQQ  
QEKARLPKIQRSEGTKRMAMYKKS LHINGGSAAEQREKIKQFSQQEEKRQKSERLQQQKQHENQMRDMLAQCESNMSEL  
QQLQNEKCHLLVEHETQKLKALDESHNQNLKEWRDKLRPRKKALEEDLNQKKREQEMFFKLSEEAECNPSTPSKAAKFF  
PYSSGDAS

Fig. 10C

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GGCCAAGACGGTCGGGGCTTGCTAACTCCAGGAACAGGTTTAAAGTTTTTGAAACTGAAGTAGGTCTACACAGTAGGA  
ACTCATGTCTATTTCTTAAGTAAACAGAGCGAATCAGCGGTCTCGGAAAGTTTCATTGTTGAGGGCTTAAGAG  
ATTTGGAACIAATTTGGAGACCAATGATGCGAGCTCAGAGTCAATAGCATCTTCTCTAAACAGGAGGTCTAGTAGCTT  
TCTGCCAGAGGGAGGGTGTACGAGCTGCTCAGTGTATAGGCAAAAGGATTTGAGGACCCTGATGACTGTGAATCTAGCAA  
GGTACAAACCAACAGGAGAGTACGTGACTGTACGGAGGATTAAACCTAGAGCTTGTTCCAATGAGATGGTAAACATTTCTTG  
CAGGGCGAGCTGCATGCTCCAAACTTTCAACCATCCCAATATCGTGCCATATCGAGCCACTTTTATTGCAGACAATGA  
GCTGTGGGTGTGCATCATTCATGGCATACGGTTCCTGCAAAAGATCTCATCTGTACACACTTCATGGATGGCATGAATG  
AGCTGGCGATTGCTTACATCTCGAGGGGTGCTGAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGT  
GTCAAAGCCAGCCACATCTCTGATCTCTGTGGATGGGAAGTCTACCTGTCTGGTTTGGCGAGCAACCTCAGCATGATAAG  
CCATGGGCAGCGGAGGTGGTCCACGATTTTCCCAAGTACAGTGTCAAGTTCTGCCGTGGCTCAGCCCCGAGGTCC  
TCCAGCAGAACTCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAACCTGGCCAAACGGC  
CATGTCCCCCTTTAAGGATATGCCCTGCCACCCAGATGCTGCTAGAGAACTGAAACGGCACAGTGGCCCTGCTGTTGGATAC  
CAGCACCATCCCCGCTGAGGAGCTGACCATGAGCCCCCTTCGGCTCAGTGGCCAACTCTGGCCTGAGTGACAGCCTGACCA  
CCAGCACCCCCGGCCCTCCAAACGGTGACTCGCCCTCCACACCCCTACCAACCGAACCTTCTCCCCCCTTCCACCACTTT  
GTGGAGCAGTGCCCTCAGCGCAACCCGGATGCCAGGCCAGTGCCAGCACCTCTCTGAACCACTCTTTCTTCAAGCAGAT  
CAAGCGACGTGCCCTCAGAGGCTTTGCCCGAATTGCTTCTGCTGTACCCCCCATCACCAATTTTGAGGGCAGCCAGTCTC  
AGGACCACAGTGGAATCTTTGGCCCTGGTAACAACTGGAAAGCTGGAGGTGGACGATTGGGAGTTCTGAGCCTCTGCA  
AACTGTGCGCATTTCTCAGCCAGGATGCAGAGGCCACCCAGAGGCCCTTCTCTGAGGGCCGCCACATTCCTCGCCCTCCT  
GGGCAGATTGGGTAGAAAGGACATTTCTCCAGGAAAGTTGACTGCTGACTGATTGGGAAAGAAATCCTGGAGAGATACT  
TCACTGCTCCAAGGCTTTTGAGACACAAAGGGAATCTCAACAACAGGGATCAGGAGGTCCAAAGCCGACATTCACAGTC  
CTGTGAGCTCAGGTGACCTCTCCGCAAGAGAGAGATGCTGCTCTGGCCCTGGGAGCTGAATTCAGGCCAGGGTTTGG  
CTCCTTAAACCCGAGGACCGCCACCTCTTCCAGTGTCTTGGACCAAGCCCTCATTTCTATTAACTTTTGCTCTCAGATGCCCT  
CAGATGCTATAGGTCAGTGAAAGGGCAAGTAGTAAGCTGCCCTCCCTTCCCTCAGACCTCTCCCTCATAAATCCAGA  
GAAGGGCATTTCTGCTTTTAAAGCACAGACTAAGGCTGGAAACAGTCCATCTTATCCCTCTTCTGGCTTGGGCCCTGAC

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Fig. 11A

ACCTAAGTCTTTCCACGGTTTATGTGTGCGCTCATTCCTTTCCACCAAGAAATCCATCTTAGCGCCTCCTGCCAGCTG  
CCCTGGTGCTTTCTCCAAGGGCCATCAGTGCTCTTGCCTAGCTTGAGGGCTTAAGTCTTTATGCTGTGTTAGTTTCGTTGT  
CAGAACAAATTAATAATTTTCAGAGACGCTG

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AAGGAAGATAAAACAAAGCCTTCTTTGGAATAGATGGATTTTGTCACTTCTGTGTGAACATAAAGTGATTCAAATGTCT  
CTTTTGGATTGCTTCTGCACCTTCAAGAACACAAAGTTGAATCACTCAGACCTGAAAAACAGTCTGAAACCAAGTATCCATCA  
ATACITGGTIGATGAGCCAAACCTTTCTCTGGTCACGTCACCTCCATCCACTAGAGCCAGTGAAGTACTATGTTCCACCAACGTTT  
CTCACTATGAGCTCCAAGTAGAAATAGGAAGAGGATTTGACAACTTGACITCTGTCCATCTTGCACGGCATACTCCCCACG  
GGAACACTGGTAACATAAAATTAACAATCTGGAAACTGCAATGAAGAACGCCCTGAAAGCTTTACAGAAAGCCGTGAT  
TCTATCCCACTTTTCCGGCATCCCAATATTACAACTTATTGGACAGTTTTCACGTGTTGGCAGCTGGCTTTGGGTTATTT  
CTCCATTTATGGCCTATGGTTCAGCAAGTCAACTCTTGAGGACCTATTTTCTGAAGGAATGAGTGAACTTTAATAAGA  
AACATTCTCTTTGGAGCCGTGAGAGGTTGAACATCTGCAACCAAAATGGCTGTATTCAAGGAGTATTAAAGCCAGCCA  
TATCCTCATTTCTGGTGTGGCCTAGTGACCCCTCTCTGGCCCTTCCCATCTGCATAGTTTGGTTAAGCATGGACAGAGGC  
ATAGGGCTGTGTATGATTTCCACAGTTCAGCACATCAGTGCAGCCGTGGCTGAGTCCAGAACTACTGAGACAGGATTTA  
CATGGGTATAATGTGAAGTCAGATATTTACAGTGTGGGATTACAGCATGTGAATTAGCCAGTGGGCAGGTGCCITTCCTCA  
GGACATGCATAGAACTCAGATGCTGTTACAGAAACTGAAAGGTCTCTTATAGCCCATTGGATATCAGTATTTTCCCTC  
AATCAGAAATCCAGAAATGAAAAATTTCCAGTCAGGTGAGACTCTGGGATTGGAGAAAGTGTGCTTGTCTCCAGTGGAACT  
CACACAGTAAATAGTGACCGATTACACACACCATCTCTCAAAACITTTCTCTCCTGCCITTTAGCTTGGTACAGCTCTG  
TTTGCAACAAGATCCTGAGAAAGGCCATCAGCAAGCAGTTTATTGTCCCATGTTTCTTCAACAGATGAAAGAAAGAA  
GCCAGGATTCAATACTTTCACTGTGCTCTCTGCTTATAACAAGCCATCAATATCATTTGCCCTCCAGTGTIACCTTGGACT  
GAGCCAGAAATGTGATTTTCTGTATTTCTCTGTATTTCTAGGTACAAATACCAGAAATTATACTTGAATAACAGTTGGT  
CTTGACACTTTCTCTGTGCTTTTCTCTGTATTTCTAGGTACAAATACCAGAAATTATACTTGAATAACAGTTGGT  
GCACITGGAGAACTCTATTATTTAAACCACTCTGTTCAAAGGGGCACCAAGTTGTAGTCCCTCTGTTTCGCACAGAGTACT  
ATGACAAGGAAACATCAGAAATTACTAATCTAGCTAGTGTCAATTTATCTGGAAATTTTCTTAAGCTGTGACTAATCTT

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Fig. 11B

TTTATCTCTCAATATAATTTTGGAGCCAGTTAAATTTTTCAGTATTTTGTCTGTCCTTGGGAATGGGCCCTCAGAGGAC  
AGTGCTTCCAAAGTACATCTTCTCCAGATCTCTGGCCCTTTTAAATGAGCTATTTGTTAAACCAACAGGCTAGTTTATCTT  
ACATCAGACCCCTTTTCTGGTAGAGGGAAAATGTTTGTCCTTTCCTTCTGTTAATACTTATGGTAAACACCTAAC  
TGAGCCCTCACTCACATTAAATGATTCACTTGAAATATATACAGAAAATGTAAATTTGCTTTTAAAAAAGGGGCTAA  
AGTAACACTTTCCTACTTATGTAAATTATAGATCCTAAATTCACGCCACCCCGTGGGAGCTCAATAAAGATTTACTGAATT

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TCAACAGGGACGATTACGAGCTGCAGGAGGTGATCGGGAGTGGAGCAACTGCTGTAGTCCAAAGCAGCTTATTGTGCCCT  
AAAAGGAGAAAAGTGGCAATCAAAACGGATAAACCTTGAGAAAATGTCAAACTAGCATGGATGAACTCCTGAAGAATAATCA  
AGCCATGAGTCAATGCCATCATCCTAATAATTGTATCTTACTACACATCTTTTGTGGTAAAGATGAGCTGTGGCTTGTCA  
TGAAAGCTGCTAAGTGGAGGTTCTGTTCTGGATATTATTAAGCACATTTGTGGCAAAAGGGGAACACAAAAAGT

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ATGGCGGGACCTGGGGCTGGAGGGACAGGGAGGTACGGGATCTGGGCCACCTGCCGGATCCAACTGGAATATTCTCACT  
AGATAAACCATTTGGCCTTGGTACTTATGGCAGAACTCTATTTGGGACITTCATGAGAAGACTGGTGCAATTACAGCTGTTA  
AAGTGATGAACGCTCGTAAGGATGAGGAAGAGGATCTCAGGACTGAACCTCAACCTTCTGAGGAAGTACTCTTCCACAAA  
AACATTTGTCTCTATGGAGCAATTTTCAAGCTGAGTCCCCCTGGTCAGCGGCCAACCTTTGGATGGTGATGGAGTT  
ATGTGCAGCAGGTTCCGTCACCTGATGTAGTGAGAAATGACCAGTAATCAGAGTTTAAAGAAGATTGGATTGCTTATATCT  
GCCGAGAAAATCCTTCAGGGCTTAGCTCACCTTCACGCCACACCGAGTAATTCACCGGGACATCAAGGTCAGAAATGTGCTG  
CTGACTCATAAATGCTGAAGTAAACTGGTTGATTTTGGAGTGAGTGGCCAGGTGAGCAGAACTAATGGAAGAAGGAATAG  
TTTCATTGGGACACCATACCTGGATGGCACCTGAGGCTGATTGACTGTGATGAGGACCCCAAGACGCTCCTATGATTACAGAA  
GTGATGTGTGCTGTGGGAATTACTGCCATTGAAATGGCTGAAGGAGCCCTCCTCTGTGTAACTTCAACCCCTTGGAA  
GCTCTCTTCGTTATTTTGGGGGAATCTGCTCCACAGTCAAAATCCAGCGGATGGTCCCGTAAGTTCACAAATTCATGGA  
AAAGTGACGATAAAAAATTTCTCTGTCCTACTTCTGCAAAACATGCTTCAACACCCCATTTGTCGGGATATAAAAA

Fig. 11C

ATGAACGACATGTTGTTGAGTCATTAAACAAGGCATCTTACTGGAATCATTAATAAAGACAGAAAAAAGAACAGGCACCG  
GAGAAAAATCAAAAGTTTCTACTCTGAGGCAAGCACCTGGCAAAAAGACTATCACCAAAAGAGGTTTCAGGGCAAAAGTCATC  
ATGGAGACCCTGAAAAGCCTTGAACCTCTCGGATTTAGAAAGCCCGCAGGCAAAAGCGCCCAACGCAGATGGGAAGATATCTTTA  
ATCAGCATGAGGAAGAAATTGAGACAAAGTTGATAAAGACAAAGAGATGAATCATCAGACAAATGATGAAGTATTTCAATTG  
ATTGAGGCTGAAGTCCAGATAGAGCCATTGAAAGCCATACATTTCAAATCTTAAATAAATTTGAGGTTCAAAGAGAGATCTCC  
TTCTGTGCCCTAACAAACAGGATCATGTCACATCATGTCAAGTTCTCTTCAAGCGTTCTCTCAGCGGTCCTCTTTTGGAAACAAG  
CTCAGAAGCCCATTTGACATCAGACAAAGGAGTTTCGCAAAATCGTCAAAATTTGGCTGGCAGCATCAGGTGATTCAAAGCAC  
AAATTTTAGCAGGCAAAACACAGAGCTACTGTTTAAACAATTATATTTCAAGAGTCAAGAAAGAAATTTCAAGAAGG  
AATGAATCAAAAGTGTACGGGAGCCCAAGTAGGATTAGGACCTGAAGGCCATTGTATTTGGCAATTTGGGTGAATCTTCTT  
CTGAGGAAGAAAGTCTGTGACTGGAAGGAGGTCTCAGTCATCACCACTTATTCTACTATTGATCAGAAAGTTGCTGGTT  
GACATCCCATGTTCCAGATGGATTTAAAGTAGGAATAATACCCCCCTGTATACITTGACAAACGAATGGGTAGGCTATAA  
TGCACTCTCTGAAATCTTCCGGAATGATTGGTTAACTCCGGCACCTGTCAATTCAGCCACCTGAAGAGGATGGTGATTATG  
TTGAACCTCTATGATGCCAGTGTGATACCTGATGGTGTGATGATGAGTCTAATGATACCTTTTGAAGATACCTATGAT  
CATGCCAATGGCAATGATGACTTGGATAACCAAGTTGATCAGGCTAATGATGTTTGTAAAGACCATGATGATGACAACAA  
TAAGTTTGTGATGATGTAAATAATAATTATTATGAGGCGCCTAGTTGTCCAAGGGCAAGCTATGGCAGAGATGGAAGCT  
GCAAGCAAGATGGTTATGATGGAAGTCTGTGGAAGAGGAAGCCTACAGAGGCTATGGAAGCCATACAGCCCAATAGAAGC  
CATGGAGGAAGTGCAGCCAGTGAGGACAAATGCAGCCATTGGAGATCAGGAAGAAACATGCAGCCCAATATAGGCAGTGAAG  
AAGAGGCAGTGAGGTTGATGGAGGTAAAGGAGTCGTTCCGAACCAAGTGAAAGAGAGTGAGCCCTTGGACTCAATGGAGAG  
AAAATTGCTCAGAGACAGATGGTCCAGGATTTGAAGAGACCTGCGTCTCAGGACCTTTGAATATCTACAGGAGGAGCCAGGT  
GGTGGAAATGAGGCCCTCAAATGCCATTGACTCAGGTGCTGCACCCGTCAAGCACCTGATCATGAGAGTGACAAATAAGGACAT  
ATCAGAAATCATCAACACAAATCAGATTTTCTGCCAATCACTCATCTCCTTCCAAGGTTCTGGGATGTCTGCTGATGCTA  
ACTTTGCCAGTGCCCATCTTATACCGCTGGATTCTGTAGAAGTACCTGAGGAATCACCTAAGCAACCCCTCTGAAGTCAATGTT  
AACCACCTCTATGCTCTCCTGCTGTAAATAAACCACTAATCCACATGTATGAAAAGGAGTTCACCTTCTGAGATCTGCTG  
TGGTTCCTTTGTGGGGAGTCAATTTGCTGTTGGGAACCCGATCTAATCTATATCTGATGGACAGAAAGTGGAAAGGCTGACA  
TTACTAAACTTATAAGGCGAAGACCATTCCGCCAGATTCAAGTCTTAGAGCCACTCAATTTGCTGATTACCATCTCAGGT

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**Fig. 11E**

GAGGTGCCCCAGCCCTGGAGTGTGGGACCCACGGCTCAGAGCCCCAGCTGGCCCCCTCCAGCCCTGCACCCCCCGCCGCC  
CCTGCTGTTCCCTGGGCCCCCTGGCCCTCACACAGCGGGAGCCACAGCGAGTATCCCATGAGCAGTTCGCGGCTGC  
CCTGCAGCTGGTGGACCCAGGCGACCCCGCTCCCTACCTGGACAACCTCATCAAGATTGGCGAGGGCTCCACGGGCA  
TCGTGTGCATCGCCACCGTGGCAGCTCGGGCAAGCTGGTGGCCGCTCAAGAAAGATGGACCTGCGCAAGCAGCAGAGGCGC  
GAGCTGCTCTTCAACGAGGTGGTAATCATGAGGGACTACACGACGAGAAATGTGGTGGAGATGTACAACAGCTACCTGGT  
GGGGACGAGCTCTGGGTGGTCAATGGAGTTCCTGGAAAGGAGCGCCCTCACCGACATCGTCACCCACACAGGATGAACG  
AGGAGCAGATCGCGCGCTGTGCTGCAAGTGTGAGGCCCTGTGCTCCACGCCAGGGCGTCAATCCACCGGGAC  
ATCAAGAGCGACTCGATCCTGCTGACCCCATGATGGCAGGGTGAAGCTGTAGACTTTGGGTTCTGCGCCACAGGTGAGCAA  
GGAAGTCCCCGAAGGAGTCTGCTGGCACGCCCTACTGGATGGCCCCAGAGCTCATCTCCGCTTCCCTACGGGC  
CAGAGGTAGACATCTGGTCTGGGGATAATGGTGAATGAGATGGTGGACGGAGAGCCCCCTACTTCAACGAGCCACCC  
CTCAAAGCCATGAAGATGATTCGGGACAACTGCCACCCCGACTGAAGAACCTGCACAAAGGTGTGCGCATCCCTGAAGGG  
CTTCTCTGACCCGCTGCTGGTGGAGACCCCTGCCAGCGGGCCACGGCAGCTGCTGAAGCACCCATTCCTGGCCA  
AGGAGGGCGCTGCCAGCATCGTGGCCCCCTCATGCGCCAGAACCGCACCATGAGGCCAGCGCCCTTCCCTCAACC  
AAAGAGCCCCCGGGTCAACCCCGCCCACTGAGGCCAGTAGGGGCCAGGCCCTCCACTCTCCAGCCCCGGGAGATG  
CTCCGCTGGCACCCCTCTTGTGGGGTAGATGAGACCCCTACTGAACCTCCAGTTTGTATCTCGTGACTTTTAG  
AAACACAGGGACTCGTGGGAGCAAGCGAGCTCCAGGACCCCACTCTGGGACAGGCCCTCCCCCATGTCTCT  
GTCTCCAGGAAGGCGAGCGCCCTCCCATCACTGGAAGTCTGCAGTGGGGTCTGCTGGGGTGGAGAGACACTAAGAGG  
TGAACATGTATGAGTGTGCACGCGTGTGAGTGTGATGTGTGTGTGTGCAAGGTCCAGCCACCCGCTCCAGC  
CCGCAAGGGGTGTCTGGCGCTTGCCCTGACACCCAGCCCCCTCTCCCCCTGAGCCATTTGTGGGGTCTGATCATGAATGC  
CGAAGAGTGGCCCTTTTCCCGTAGCCCTGCGCCCCCTTCTGTGGCTGGAATGGGGAGACAGGTCAAGGCCCTCCACCTCT  
CCAGCCCCCTGCAGCAATGACTACTGCACCTGGACAGCCCTCTCTTTCTAGAACTCTATTTATATTGTCAATTTATAC  
ACTTAGCCCCCTGCCCCCTTATTGGGGGACAGATGGTCCCTGTCTGCGGGGTGGCCCTGGCAGAACCACTGCTGAAGAAC  
CAGGTTCTGCCCCGCTCAGCGCAGCCCCAGCCCCACCCCTGCTCGAGTTAGTTTACAAATTAAACATTTGTCTTGT  
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CGAAGCCACAGCCCGAGCCCGAGCCCGGCGGCCACCGCGCCCCCGGCCCATGGCTTTTGCCCAATTTCCGGCC  
GCATCCTGCGCCTGTCTACCTTCGAGAAAGAGAAAGTCCCGCGAATAATGAGCACGTCCGCGCGGACCTGGACCCCAACGAG  
GTGTGGGAGATCGTGGCGGAGCTGGCGGACGCGCCTTCGGCAAGGTTTACAAGGCCAAGAAATAAGGAGACGGGTGCTTT  
GGCTGGGGCCCAAAGTCAATTGAACCAAGAGTGAGGAGGAGCTGGAGGACTACATCGTGGAGATTGAGATCCTGGCCACCT  
GGGACCAACCCCTACATTGTGAAGCTCCTGGGAGCCTACTATCACGACGGGAAGCTGTGGATCATGATTGAGTTCTGTCCA  
GGGGAGCCGTGGACGCCATCATGTCTGGAGCTGGACAGAGGCCCTCACGGAGCCCCAGATACAGGTGGTTTGGCCGCCAGAT  
GCTAGAAGCCCTCAACTTCCTGCACAGCAAGAGGATCATCCACCGAGATCTGAAGCTGGCAACGTGCTGATGACCCCTCG  
AGGGAGACATCAGGCTGGCTGACTTTGGTGTCTGCTGCCAAGAACTCTGAAGACTTACAGAAACGAGATTCTTTCATCGGC  
ACGCCTTACTGGATGGCCCCCGAGGTGGTCAATGTGTGAGACCATGAAGACACGCCCTACGACTACAAAGCCGACATCTG  
GTCCCTGGGCATCACGCTGATTGAGATGGCCCCAGATCGAGCCGCCACACACGAGCTCAACCCCATGCGGGTCTCTGCTAA  
AGATCGCCCAAGTCGGACCCCTCCACGCTGCTCACGCCCTCCCAAGTGGTCTGTAGAGTTCCGTGACTTCTTGAAGATAGCC  
CTGGATAAGAACCCAGAACCCGACCCAGTGGCCGCGAGCTGCTGGAGCATCCCTTCGTACGACGATCACACAGTAACAA  
GGCTCTGCGGGAGCTGGTGGCTGAGGCCAAGGCCGAGGTGATGGAAGAGATCGAAGACGGCCGGGATGAGGGGGAAAGAGG  
AGGACGCCGTGGATGCCGCCCTCCACCCCTGGAGAACCATACTCAGAACTCCTCTGAGGTGAGTCCGCCAAGCCTCAATGCT  
GACAAAGCCTCTCGAGGAGTCACTTCCACCCCGCTGGCACCCAGCCAGTCTCAGGACAGTGTGAATGAGCCCTGCAGCCA  
GCCCTCTGGGGACAGATCCCTCCAAACCAACCACTCCAGTCCCCAGTCTGGCCCTTGGAAATGAGAACGGCCTGGCAGTGCCTG  
TGCCCCCTGCGGAAGTCCCGACCCGTGTCAATGGATGCCAGAAATTCAGGTAGCCCAAGGAGAACAGTTGCTGAGCAGGGT  
GGGGACCTCAGCCAGCAGCCAAACAGATCTCAAAGGCCAGCCAGAGCCGCCCAACAGCAGCGCCCTGGAGACCTTGGG  
TGGGGAGAAAGCTGGCCCAATGGCAGCCTGGAGCCACCTGGCCAGGCAGCTCCAGGGCCTTCCAAGAGGGACTCGGACTGCA  
GCAGCCTCTGCACCTCTGAGAGCATGGACTATGGTACCAATCTCTCCACITGACCCTGTGCTGAACAAGAGATGGGCTCT  
CTGTCCATCAAGGACCCGAAACTGTACAAAACCCCTCAAGCGGACACGCCAAATTTGTGGTGGATGGTGTGGAGGTGAG  
CATCACCACTCCAAGATCATCAGCGAAGATGAGAAGAAAGGATGAGGAGATGAGATTCTCAGGGCCAGGAACCTCCGAG  
AGCTTCGGCTGCTCCAGAAAGAGGATCGGAACCCAGACCCAGCTGAGTAACAAGCATGAGCTGCAGCTGGAGCAAAATG  
CATAAACGTTTTGAACAGGAAATCAACGCCCAAGAAAGATTCTTTGACACGGAAATTAGAGAACCTGGAGCGTCAAGCAAA

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Fig. 11G



GCAGCAAGTGGAGAAGATGGAGCAAGACCATGCCGTGCGCCGCGGGAGGAGGCCAGGGCGGATCCGCCCTGGAGCAGGATC  
GGGACTACACCAGGTTCCAAAGAGCAGCTCAAACTGATGAAGAAAGAGGTGAAGAACGAGGTGGAGAAAGCTCCCCGACAG  
CAGCGGAAGGAAGCATGAAGCAGAAAGATGGAGGAGCACACGCAAGAAAGCAGCTTCTTGACCCGGGACTTTGTAGCCAA  
GCAGAAAGGAGGACCTGGAGCTGGCCATGAAGAGGCTACCAACGACAAACAGGCGGGAGATCTGTGACAAAGGAGCGCGAGT  
GCCCTCATGAAGAAAGCAGGAGCTCCTTCGAGACCGGGAAGCAGCCCTGTGGGAGATGGAAAGACCAAGCTGCAGGAGAGG  
CACCAAGCTGGTGAAGCAGCAGCTCAAAGACCAGTACTTCCTCCAGCGGCACGAGCTGCTGCGCAAGCATGAGAAGGAGCG  
GGAGCAGATGCAGCGCTACAACAGCGCATGATAGAGCAGCTGAAGGTGCGGCAGCAACAGGAAAGGCGGCTGCCCA  
AGATCCAGAGGAGTGAGGGCAAGACGCGCATGGCCATGTACAAGAAAGAGCTCCACATCAACGGCGGGGCGAGCGCAGCT  
GAGCAGCGTGAGAAGATCAAGCAGTTCTCCAGCAGGAGGAGAAAGAGGCGGCTGCGAGCGGCTGCAGCAACAGCAGAA  
ACACGAGAACCCAGATGCGGGACATGCTGGCGCAGTGCGGAGCAACATGAGCGAGCTGCAGCAGCTGCAGAAATGAAAGT  
GCCACCTCCTGTAGACACGAAACCCAGAACTGAAGGCCCTGGATGAGAGCCATAACCAAGAACCTGAAGGAATGGCGG  
GACAAAGCTTCGGCCCGCAAGAGGCTCTGGAAGAGGATCTGAACCAAGAAAGCGGAGCAGGAGATGTTCTTCAAGCT  
GAGCGAGGAGCGGAGTGCCCCAACCCCTCCACCCCAAGCAAGGCCCAAGTTCTTCCCTACAGCTCTGGGGATGCTT  
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Fig. 11H

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STLK6_h	G	P	P	Y	S	P	L	D	I	S	I	F	P	Q	S	E	S	R	M	K	N	S	Q	S	G	V	D	S	G	I	G	E	S	V	L	V	S	S	G	T	H	T	V	N	S	D	R	L	H	T	332																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
STLK5_h	G	T	V	P	C	L	L	D	T	S	T	I	P	A	E	E	L	T	M	S	P	S	R	S	V	A	N	S	G	L	S	D	S	-	L	T	T	S	T	P	R	P	S	N	G	D	S	P	S	H	249																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
SPAK_h	N	D	P	P	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-


Fig. 12B

PAK1_h U51120	MSNNGLDIQDKPPAPPMRNTSTMIGAGSKDAGTLNHGSKPLPPNPEEKKKKDRFYRSILP	60
PAK4_h	-----	0
PAK5_h	-----	0
PAK1_h U51120	GDKTNKKKEKERPEISLPSDFEHTIHVGFDAVT-GEFTGMPEQWARLQTSNITKS	115
PAK4_h	---MFRKKKKKKRPEISAPQNFQHRVHTSFDPKEGKFVGLPPQWQNIID-ILRRPKPVVDP	56
PAK5_h	---MF-GKRKKRVIEISAPSNFEHRVHTGFDQHEQKFTGLPRQWQSLIEFSARRPKPLVDP	56
PAK1_h U51120	-----	115
PAK4_h	SRITRVQLQPMKTVVRGSAAMPVDGYTSGLLNDIQKLSVISNTLRGRSPTSRRAQSLGL	116
PAK5_h	ACITSIQPGAPKTIIVRGSKGAKDGAITLLDEFFENMSVTRSNLRRDSPPPARAR	112
PAK1_h U51120	-----	115
PAK4_h	LGDEHWATDPDMYLQSPQSERTDPHGLYLSGNGGTPAGHKQMPWPEPQSPRVLPNGLAAK	176
PAK5_h	-----QENGMPPEEPATTARGGPCK	131
PAK1_h U51120	-----	127
PAK4_h	AQSLGPAEFQGAQRCLQLGACLQSSPPGASPPPTGTNRHGMKA AKHGSSEARPSCLVGS	236
PAK5_h	AGSRGR-----FAGHSEAGGSGDRRRAAGPEKRPKSSREGSGGPQESSRDKRP--LSGP	183
PAK1_h U51120	LEFY-N SKKTNSQKYMSTDKS-----AEDYNSSNALNVKA-----VSETPAVPPVS	174
PAK4_h	ATGRPGGEGSPSPKTRESSLKRLFRSMFLSTAAITAPSSSKPKPPQSKPNSSFRPPQK	296
PAK5_h	DVGTPOPAGLASGAKLAAG-----RPFNTYPRADTDHPSTRCAQGEPHDVA PNGP-----	232

Fig. 13A

**Fig. 13B**

PAK1_h	U51120	Q	H	Q	F	L	K	I	A	K	P	L	S	L	T	P	L	I	A	A	K	E	A	T	K	N	N	H	545	
PAK4_h		D	H	P	F	L	I	Q	T	G	L	P	E	C	L	V	P	L	I	Q	L	Y	R	K	Q	T	S	T	C	681
PAK5_h		K	H	P	F	L	A	K	A	G	P	P	A	S	T	V	P	L	M	R	Q	N	R	I	R					591

 RESIDUES THAT MATCH THE CONSENSUS NAMED CONSENSUS #1 EXACTLY.


 BOX RESIDUES THAT MATCH THE CONSENSUS EXACTLY.

Fig. 13C

ZC4_h.pro	MAGPGGWRDREVTDLGHLPDPTGIFSLDKTIIGLGTYGRIYGLGHEKGTGAF	50
ZC1_h.pro	MANDSPAKSLVDIDLSSLRDPAGIFEELVEVVGNGTYGQVYKGRHVKTGQL	50
ZC4_h.pro	TAVKVMNARKDEEEDLRTIELNLLRKYSFHKNIVSFYGAFFKLSPPGQRHQ	100
ZC1_h.pro	AAIKVMDVTEDEEEEEKLEINMLKKYSHHNRINIAITYYGAFIKKSPPGHDDQ	100
ZC4_h.pro	LWMVME LCAAGSVTDVVRMTSNQSLKEDWIAIYICREILQGLAHLHAHRVI	150
ZC1_h.pro	LWLVMEEFCGAGSITDLVKNTKGNLTLKEDWIAIYSREILRGLAHLHIHVI	150
ZC4_h.pro	HRDIKGQNVLLTHNAEVKLVDFGVSAQVSRITNGRRNSFIGTPTYWMAPEVI	200
ZC1_h.pro	HRDIKGQNVLLTENA EVKLVDFGVSAQLDRTVGRRTFIGTPTYWMAPEVI	200
ZC4_h.pro	DCDEDPRRSYDYRS D VWSVGITAIEMAEGAPPLCNLQPLEALFVILRESA	250
ZC1_h.pro	ACDENPDATYDYRS D LWS CGITAIEMAEGAPPLCDMHPMRALFLIPRNP	250
ZC4_h.pro	PTVKSSGWSRKFFHNFMEKCTIKNFLFRPTSANMLQHPFVVDIKNERHVVE	300
ZC1_h.pro	PRLKSKKWSKKFFSFTIEGCLVKNYMQRPSTEQLKHPFIIRDQPNRQVRI	300
ZC4_h.pro	SLTRHLTGIKKR-----OKKEQAREKKS	324
ZC1_h.pro	QLKDHIDRTRKRRGEKDETEYEYSGSEEEEEVEPEGEPESSIVNVPGES	350
ZC4_h.pro	KVSTLRQALAKRLSPKKRFRACKSSWRPEKLELSDLEARRQRRQRWEDIFN	374
ZC1_h.pro	TLRDRLRLQQENKERSEALRRRQQLLQEQQLREQEEYKRQLLAERQKRIE	400
ZC4_h.pro	QHEEELROVDKDKEDESSNDDEVFHSIOAEVQIEPLKPYISNPKKIEVQE	424
ZC1_h.pro	QQKEQRRRLLEEQQRREREARRQREQEREQRRREQEEKRRLEELERRRKEEEE	450

Fig. 14A

ZC4_h.pro	RSPV	NNQD	HAHV	KFS	SV	PQRS	LL	EQ	AQ	KPI	D	IR	QR	SS	QN	RQ	NW	LAA	474																																
ZC1_h.pro	RR	AA	EE	KRR	V	ERE	Q	EY	IR	RQ	LE	EE	QR	H	EV	LQ	QQL	Q	EQ	AM	LL	EC	R	W	RE	500																									
ZC4_h.pro	SG	DS	KH	KI	L	AG	KT	Q	S	Y	CL	T	I	Y	I	S	E	V	K	K	E	E	F	Q	E	G	M	N	Q	K	C	Q	G	A	Q	V	G	L	G	P	E	G	H	524							
ZC1_h.pro	M	E	E	H	R	Q	A	E	R	L	Q	R	Q	L	Q	E	A	Y	L	L	S	L	Q	H	D	H	R	R	P	H	P	Q	H	S	Q	Q	P	P	P	Q	Q	E	R	S	K	P	S	550			
ZC4_h.pro	C	I	W	Q	L	G	E	S	S	S	E	E	E	S	P	V	T	G	R	R	S	Q	S	S	P	P	Y	S	T	I	D	Q	K	L	L	V	D	I	H	V	P	D	G	F	K	V	G	K	I	S	574
ZC1_h.pro	F	H	A	P	E	P	K	A	H	Y	E	P	A	D	R	A	R	E	V	E	D	R	F	R	K	T	N	H	S	S	P	E	A	Q	S	K	Q	T	G	R	V	L	E	P	P	V	P	S	R	S	600
ZC4_h.pro	P	P	V	Y	L	T	N	E	W	V	G	Y	N	A	L	S	E	I	F	R	N	D	W	L	T	P	A	P	V	I	O	P	P	E	E	D	G	D	Y	V	E	L	Y	D	A	S	A	D	I	D	624
ZC1_h.pro	E	S	F	S	N	G	N	S	E	S	V	H	P	A	L	Q	R	P	A	E	P	Q	V	P	V	R	T	S	R	S	P	V	L	S	R	R	D	S	P	L	Q	G	S	G	Q	N	S	Q	650		
ZC4_h.pro	G	D	D	D	E	S	N	D	T	F	E	D	T	Y	D	H	A	N	G	N	D	D	L	D	N	Q	V	D	Q	A	N	D	V	C	K	D	H	D	D	N	K	F	V	D	D	V	N	674			
ZC1_h.pro	A	G	Q	R	N	S	T	S	I	E	P	R	L	L	W	E	R	V	E	K	L	V	P	R	P	G	S	G	S	S	G	S	S	S	G	S	S	G	S	P	G	S	H	P	G	S	Q	S	G	S	700
ZC4_h.pro	N	N	Y	E	A	P	S	C	P	R	A	S	Y	G	R	D	G	S	C	K	Q	D	G	Y	D	G	S	R	G	K	E	E	A	Y	R	G	Y	G	S	H	T	A	N	R	S	H	G	G	S	724	
ZC1_h.pro	G	E	R	F	R	V	R	S	S	S	K	S	E	G	S	P	S	Q	R	L	E	N	A	V	K	P	E	D	K	E	V	F	R	P	L	K	P	A	D	L	T	A	L	A	K	E	L	R	750		
ZC4_h.pro	A	A	S	E	D	N	A	I	G	D	Q	E	E	H	A	N	I	G	S	E	R	R	G	S	E	G	D	G	G	K	G	V	V	R	T	S	E	E	S	G	A	L	G	L	N	G	E	E	774		
ZC1_h.pro	A	V	E	D	V	R	P	P	H	K	V	T	D	Y	S	S	S	E	S	G	T	T	D	E	E	D	D	V	E	Q	E	G	A	D	E	S	T	S	G	P	E	D	T	R	A	A	S	800			
ZC4_h.pro	N	C	S	E	T	D	G	P	G	L	K	R	P	A	S	O	D	F	E	Y	L	Q	E	E	P	G	G	N	E	A	S	N	A	I	D	S	G	A	P	S	A	P	D	H	E	S	D	N	824		
ZC1_h.pro	S	L	N	L	S	N	G	E	T	E	S	V	K	T	M	I	V	H	D	D	V	E	S	E	P	A	M	T	P	S	K	E	G	T	L	I	V	R	R	T	Q	S	A	S	S	T	L	Q	K	H	850
ZC4_h.pro	K	D	I	S	E	S	T	O	S	D	F	S	A	N	H	S	P	S	K	G	S	G	M	S	A	D	A	N	F	A	S	A	I	L	Y	A	G	F	V	E	V	P	E	E	S	P	K	Q	874		
ZC1_h.pro	K	S	S	S	F	T	P	F	I	D	P	R	L	L	Q	I	S	P	S	S	G	T	T	V	T	S	V	V	G	E	S	C	D	G	M	R	P	E	-	-	A	I	R	Q	D	P	T	R	K	898	

Fig. 14B



ZC4_h.pro	PSEVNVNPLYVSPACKKPLIHMYEKEFTSEICCGSLWGVNLLLGTRSNLY	924
ZC1_h.pro	GSVVNVNPTNTRPQSDTPEIRKYKKRFNFSEILCAALWGVNLLVGTESGLM	948
ZC4_h.pro	LMDRSGKADITKLIRRRPFRQIQVLEPLNLLITISGHKNRRLRVYHLTWLR	974
ZC1_h.pro	LLDRSGQGKVPYPLINRRRFQQMDVLEGLNVLVITISGKKDKLKVYVYLSWLR	998
ZC4_h.pro	NKILNNDPESKRRQE-EMLKTEEACKAIDKLTGCEHFSVLQHEETIYIAI	1023
ZC1_h.pro	NKILHNDPEVEKKQGW-TVGDLFGCVHYKVVKYERIKFLVI	1039
ZC4_h.pro	ALKSSIHLAYAWAPKSFDESTAIKVFPITLDHKPVTVDLAIGSEKRLKIFFS	1073
ZC1_h.pro	ALKSSVEVYAWAPKPYHKFMAFKSEFGEIVHKPLLVDLTVEEGQRLKVIYG	1089
ZC4_h.pro	SADGYHLIDAEESEVMSDVITLPKNPLEIIPQNIILPDCLGIGMMLTFNA	1123
ZC1_h.pro	SACGFHADVDSGSVYDIYLPHTHIQCSIKPHAIIILPNTDGMELLVCYED	1139
ZC4_h.pro	EALSVANEQLFKKILEMWKDIPSSIAFECTORITGWGOKAIEVRSLSQSR	1173
ZC1_h.pro	EGVYVNTYGRITKDDVVLQWIGEMPTSVAYIRSNQIMGWGEKAIETRSVETG	1189
ZC4_h.pro	VLESELKRRSIIKKLRFCLCTRGDKLFFTSILRNHHSRVYFMTLGKLEELQS	1223
ZC1_h.pro	HLDGVFMHKRAQRLLKFLCERNDKVFFASVRSGGSSQVYFMTLGRSLLSW	1239
ZC4_h.pro	NYDV	1227
ZC1_h.pro		1239

BOX RESIDUES THAT MATCH ZC4\_h.pro EXACTLY.

Fig. 14C

Db = LOK1\_m

Qy = GEK2\_h

```
*****
*****
1 1MAFANFRRI LRLSTFEKRKSREYEHVRRDLDPNDVWEIVGELGDGAFGKVKYKAKNKETGA 60
Qy 1MAFANFRRI LRLSTFEKRKSREYEHVRRDLDPNEVWEIVGELGDGAFGKVKYKAKNKETGA 60

*****
*****
61 1LAAKV IETKSEEELEDYIVEIEILATCDHPYIVKLLGAYYDGGKLIWIMIEFCPGGAVDA 120
Qy 61 1LAAKV IETKSEEELEDYIVEIEILATCDHPYIVKLLGAYYHDGKLIWIMIEFCPGGAVDA 120

*****
*****
121 1MLELDRGLTEPQIQVVC RQMLEALNFLHGKR I IHRDLKAGNVLMTLEGD IRLADFGVSA 180
Qy 121 1MLELDRGLTEPQIQVVC RQMLEALNFLHSKR I IHRDLKAGNVLMTLEGD IRLADFGVSA 180

*****
*****
181 1KNLKT LQKRDSFIGTPYWM APEVVLCE TMKDAPYDYKADIWSLGITL IEMAQIEPPHHEL 240
Qy 181 1KNLKT LQKRDSFIGTPYWM APEVVMCE TMKDTPTYDYKADIWSLGITL IEMAQIEPPHHEL 240

*****
*****
241 1NPMRVLLKIAKSDPPTLLTPSKWSVEFRD FLKIALDKNPETRP SAAQLLQHPFVSRVTSN 300
Qy 241 1NPMRVLLKIAKSDPPTLLTPSKWSVEFRD FLKIALDKNPETRP SAAQLLLEHPFVSSITSN 300

*****
*****
301 1KALRELVAEAKAEVMEEIEDGRDEGE EEDAVDAASTLENHTQNSSEVSPPSLNADKPLEE 360
Qy 301 1KALRELVAEAKAEVMEEIEDGRDEGE EEDAVDAASTLENHTQNSSEVSPPSLNADKPLEE 360
```

Fig. 15A



\*\*\*\*\*  
Db 720 ICDKERDCLSKKQELLRDREAALWEMEEHQLQERHQLVKQQLKDQYFLQRHDLRKKHEKE 779  
Qy 721 ICDKERECLMKKQELLRDREAALWEMEEHQLQERHQLVKQQLKDQYFLQRHELRLKKHEKE 780  
  
\*\*\*\*\*  
Db 780 REQMQRYNQRMMEQLKVRQQQEKARLPKIQRS DGETRMAMYKKS LHINGAGSASEQREKI 839  
Qy 781 REQMQRYNQRMIEQLKVRQQQEKARLPKIQRSEKTRMAMYKKS LHINGGGSAAEQREKI 840  
  
\*\*\*\*\*  
Db 840 KQFSQQ'E EK RQKAERLQQQKHEHQMRDMVAQCESNMSELQQ LQNEKCYLLVEHETQKLK 899  
Qy 841 KQFSQQ'E EK RQKSERLQQQKHEHQMRDMLAQCESNMSELQQ LQNEKCHLLVEHETQKLK 900  
  
\*\*\*\*\*  
Db 900 ALDESHNQSLKEWRDKLRPRKKALEEDLNQKKREQEMFFKLSEEA E-PRPTTPSKASNFF 958  
Qy 901 ALDESHNQNLKEWRDKLRPRKKALEEDLNQKKREQEMFFKLSEEA ECPNPSTPSKA AKFF 960  
  
\*\*\*\*\*  
Db 959 PYSSGDAS 966  
Qy 961 PYSSGDAS 968

Fig. 15C